

89	365	29.0	207	14	US-10-154-678-54	Sequence 54, Appl	162	250	19.9	220	14	US-10-131-409-24	Sequence 24, Appl
90	362.5	28.8	166	9	US-09-759-143-838	Sequence 838, App	163	250	19.9	220	15	US-10-150-811-24	Sequence 24, Appl
91	362.5	28.8	166	9	US-09-780-669-838	Sequence 838, App	164	249	19.8	220	15	US-10-150-811-98	Sequence 98, Appl
92	362.5	28.8	166	9	US-09-822-827-838	Sequence 838, App	165	249	19.8	220	15	US-10-139-854-98	Sequence 98, Appl
93	362.5	28.8	166	9	US-09-895-793-838	Sequence 838, App	166	249	19.8	220	15	US-10-131-409-98	Sequence 98, Appl
94	362.5	28.8	166	9	US-09-895-814-838	Sequence 838, App	167	249	19.8	220	15	US-10-150-811-98	Sequence 98, Appl
95	362.5	28.8	166	13	US-10-012-896-838	Sequence 838, App	168	241.5	19.2	220	15	US-10-357-175-22	Sequence 22, Appl
96	362.5	28.8	166	14	US-10-144-678A-838	Sequence 838, App	169	241.5	19.2	220	15	US-10-455-720-22	Sequence 22, Appl
97	362.5	28.8	166	14	US-10-294-025-838	Sequence 838, App	170	236.5	18.8	220	15	US-09-888-615-93	Sequence 93, Appl
98	361.5	28.7	228	15	US-10-156-214A-272	Sequence 272, App	171	232.5	18.5	220	15	US-10-074-978A-220	Sequence 220, App
99	361	28.7	151	14	US-10-357-175-21	Sequence 21, Appl	172	231	18.4	220	15	US-09-910-151-4	Sequence 4, Appl
100	361	28.7	151	15	US-10-455-720-21	Sequence 21, Appl	173	231	18.4	220	15	US-10-174-333-157	Sequence 157, App
101	360.5	28.7	228	14	US-10-203-676-6	Sequence 6, Appl	174	225	17.9	200	12	US-10-150-813-96	Sequence 96, Appl
102	360	28.6	199	9	US-09-759-143-172	Sequence 172, App	175	224	17.8	197	12	US-10-139-854-96	Sequence 96, Appl
103	360	28.6	159	9	US-09-780-669-172	Sequence 172, App	176	224	17.8	197	12	US-10-131-409-96	Sequence 96, Appl
104	360	28.6	159	9	US-09-030-606-172	Sequence 172, App	177	224	17.8	197	15	US-10-150-811-96	Sequence 96, Appl
105	360	28.6	159	9	US-09-822-827-172	Sequence 172, App	178	220	17.5	159	14	US-10-357-175-24	Sequence 24, Appl
106	360	28.6	159	9	US-09-115-453-172	Sequence 172, App	179	220	17.5	159	15	US-10-455-720-24	Sequence 24, Appl
107	360	28.6	159	9	US-09-232-880-172	Sequence 172, App	180	218.5	17.4	164	9	US-09-759-143-178	Sequence 178, App
108	360	28.6	159	9	US-09-895-793-172	Sequence 172, App	181	218.5	17.4	164	9	US-09-800-669-178	Sequence 178, App
109	360	28.6	159	9	US-09-895-814-172	Sequence 172, App	182	218.5	17.4	164	9	US-09-030-606-178	Sequence 178, App
110	360	28.6	159	13	US-10-012-896-172	Sequence 172, App	183	218.5	17.4	164	9	US-09-822-827-178	Sequence 178, App
111	360	28.6	159	14	US-10-010-940-172	Sequence 172, App	184	218.5	17.4	164	9	US-09-115-453-178	Sequence 178, App
112	360	28.6	159	14	US-10-144-678A-172	Sequence 172, App	185	218.5	17.4	164	9	US-09-232-880-178	Sequence 178, App
113	360	28.6	159	14	US-10-294-025-172	Sequence 172, App	186	218.5	17.4	164	9	US-09-895-793-178	Sequence 178, App
114	349	27.7	161	12	US-10-344-394-8	Sequence 8, Appl	187	218.5	17.4	164	9	US-09-895-814-178	Sequence 178, App
115	344.5	27.4	133	15	US-10-264-049-3307	Sequence 3307, Ap	188	218.5	17.4	164	13	US-10-012-896-178	Sequence 178, App
116	339.5	27.0	214	9	US-09-815-876-4	Sequence 4, Appl	189	218.5	17.4	164	14	US-10-010-940-178	Sequence 178, App
117	339	26.9	144	9	US-09-796-294-1	Sequence 1, Appl	190	218.5	17.4	164	14	US-10-144-678A-178	Sequence 178, App
118	339	26.9	144	14	US-10-461-787-1	Sequence 1, Appl	191	218.5	17.4	164	14	US-10-357-175-25	Sequence 25, Appl
119	339	26.9	146	9	US-09-796-294-3	Sequence 3, Appl	192	218.5	17.4	164	14	US-10-294-025-178	Sequence 25, Appl
120	339	26.9	146	14	US-10-461-787-3	Sequence 3, Appl	193	218.5	17.4	164	15	US-10-455-720-25	Sequence 25, Appl
121	338.5	26.9	229	10	US-09-898-837A-53	Sequence 53, Appl	194	216.5	17.2	203	15	US-10-074-566-118	Sequence 118, App
122	327	26.0	119	12	US-10-262-511-54	Sequence 54, Appl	195	215.5	17.1	154	14	US-10-029-386-32241	Sequence 32241, A
123	327	26.0	142	12	US-10-262-511-48	Sequence 48, Appl	196	214	17.0	154	14	US-10-357-175-23	Sequence 23, Appl
124	327	26.0	148	12	US-10-262-511-52	Sequence 52, Appl	197	214	16.9	157	15	US-10-455-720-23	Sequence 23, Appl
125	325.5	25.9	102	12	US-10-262-511-56	Sequence 56, Appl	198	212.5	16.3	192	11	US-09-997-003-39	Sequence 39, Appl
126	320	25.4	224	16	US-10-408-765A-345	Sequence 345, App	199	204.5	16.3	192	9	US-09-935-297-529	Sequence 529, App
127	319	25.4	144	9	US-09-796-294-4	Sequence 4, Appl	200	203.5	16.2	135	14	US-10-148-671-24	Sequence 24, Appl
128	319	25.4	144	14	US-10-461-787-4	Sequence 4, Appl	201	202	16.1	222	9	US-09-812-197-5	Sequence 5, Appl
129	316.5	25.2	119	12	US-10-262-511-60	Sequence 60, Appl	202	202	16.1	222	14	US-10-162-742-5	Sequence 5, Appl
130	315.5	25.1	286	16	US-10-408-765A-353	Sequence 353, App	203	200	15.9	228	12	US-10-174-333-107	Sequence 107, App
131	303.5	24.1	140	12	US-10-247-703-18	Sequence 18, App	204	199	15.8	98	14	US-10-174-333-2	Sequence 2, Appl
132	295.5	23.5	176	16	US-10-408-765A-2795	Sequence 2795, Ap	205	198.5	15.8	159	14	US-10-240-730-2	Sequence 2, Appl
133	295.5	23.5	163	12	US-10-247-703-12	Sequence 12, Appl	206	198	15.7	159	14	US-09-796-294-5	Sequence 5, Appl
134	295.5	23.5	176	12	US-10-247-703-14	Sequence 14, Appl	207	198	15.7	159	14	US-10-461-787-5	Sequence 5, Appl
135	295.5	23.5	180	15	US-10-341-434-36	Sequence 36, Appl	208	195.5	15.5	187	12	US-10-262-511-50	Sequence 5, Appl
136	294.5	23.4	144	10	US-09-860-739-2	Sequence 2, Appl	209	195.5	15.5	187	13	US-09-804-156-17	Sequence 17, Appl
137	293.5	23.3	182	12	US-10-307-817-148	Sequence 148, App	210	195.5	15.5	187	13	US-10-125-459-9	Sequence 9, Appl
138	285	22.7	181	9	US-09-864-761-46600	Sequence 46600, A	211	195.5	15.5	187	13	US-10-067-761-17	Sequence 17, Appl
139	284.5	22.6	222	15	US-10-423-311-1	Sequence 1, Appl	212	195.5	15.5	187	14	US-10-319-519-17	Sequence 17, Appl
140	281.5	22.4	206	10	US-09-898-837A-42	Sequence 42, Appl	213	194	15.4	59	12	US-10-262-511-58	Sequence 58, Appl
141	278	22.1	121	14	US-10-344-394-7	Sequence 7, Appl	214	193.5	15.4	217	9	US-09-755-016-2	Sequence 2, Appl
142	276.5	22.0	169	14	US-10-106-698-6322	Sequence 6322, Ap	215	184.5	14.7	164	9	US-09-735-713A-6	Sequence 6, Appl
143	276.5	22.0	227	9	US-09-888-615-84	Sequence 84, Appl	216	184	14.6	54	10	US-09-860-739-5	Sequence 5, Appl
144	268.5	21.3	193	12	US-10-243-558-890	Sequence 890, App	217	182	14.5	66	14	US-10-316-253-80	Sequence 80, Appl
145	266.5	21.2	217	14	US-10-106-698-4740	Sequence 4740, Ap	218	179	14.2	97	12	US-10-262-511-100	Sequence 100, App
146	257	20.4	133	9	US-09-925-297-642	Sequence 642, App	219	177.5	14.1	172	12	US-10-174-333-155	Sequence 155, App
147	256.5	20.4	218	9	US-09-861-708-3	Sequence 3, Appl	220	177	14.1	217	14	US-10-376-345-4	Sequence 4, Appl
148	255.5	20.3	227	16	US-10-275-505-7	Sequence 7, Appl	221	174	13.8	77	9	US-09-759-143-329	Sequence 329, App
149	254.5	20.3	227	14	US-10-384-474-8	Sequence 8, Appl	222	174	13.8	77	9	US-09-780-669-329	Sequence 329, App
150	254.5	20.2	199	15	US-10-423-311-2	Sequence 2, Appl	223	174	13.8	77	9	US-09-822-827-329	Sequence 329, App
151	253.5	20.2	218	16	US-10-408-765A-87	Sequence 87, Appl	224	174	13.8	77	9	US-09-822-880-329	Sequence 329, App
152	250	19.9	203	12	US-10-150-813-95	Sequence 95, Appl	225	174	13.8	77	9	US-09-895-793-329	Sequence 329, App
153	250	19.9	203	12	US-10-139-854-95	Sequence 95, Appl	226	174	13.8	77	9	US-09-895-814-329	Sequence 329, App
154	250	19.9	203	14	US-10-131-409-95	Sequence 95, Appl	227	174	13.8	77	13	US-10-012-896-329	Sequence 329, App
155	250	19.9	203	15	US-10-150-811-95	Sequence 95, Appl	228	174	13.8	77	14	US-10-010-940-329	Sequence 329, App
156	250	19.9	205	12	US-10-150-813-97	Sequence 97, Appl	229	174	13.8	77	14	US-10-144-678A-329	Sequence 329, App
157	250	19.9	205	12	US-10-139-854-97	Sequence 97, Appl	230	174	13.8	77	14	US-10-294-025-329	Sequence 329, App
158	250	19.9	205	14	US-10-131-409-97	Sequence 97, Appl	231	174	13.8	77	14	US-10-394-025-329	Sequence 177, Appl
159	250	19.9	205	15	US-10-150-811-97	Sequence 97, Appl	232	170.5	13.6	130	12	US-10-174-333-177	Sequence 18, Appl
160	250	19.9	220	12	US-10-150-813-24	Sequence 24, Appl	233	169	13.4	219	9	US-09-804-156-18	Sequence 18, Appl
161	250	19.9	220	12	US-10-139-854-24	Sequence 24, Appl	234	169	13.4	219	13	US-10-067-761-18	Sequence 18, Appl

235	169	13.4	219	14	US-10-319-519-18	Sequence 18, Appl	308	96	7.6	73	14	US-10-357-175-158	Sequence 158, Appl
236	168	13.2	120	14	US-10-332-122-4	Sequence 4, Appl	309	95	7.6	35	9	US-09-885-441-3	Sequence 3, Appl
237	165.5	13.4	116	12	US-10-424-599-236797	Sequence 236797, A	310	95	7.6	35	12	US-10-424-836-3	Sequence 3, Appl
238	165	13.1	223	15	US-10-108-260A-4500	Sequence 4500, A	311	95	7.6	56	9	US-09-864-761-44838	Sequence 44838, A
239	156.5	12.4	97	12	US-09-825-751A-8	Sequence 8, Appl	312	95	7.6	56	9	US-09-864-761-45193	Sequence 45193, A
240	152.5	12.1	140	12	US-10-424-599-157545	Sequence 157545, A	313	93	7.4	38	9	US-09-910-151-9	Sequence 9, Appl
241	148.5	11.8	183	12	US-10-424-599-263901	Sequence 263901, A	314	92.5	7.4	90	15	US-10-074-566-119	Sequence 119, Appl
242	147	11.7	80	12	US-10-296-115-1294	Sequence 1294, A	315	92.5	7.4	90	15	US-10-074-566-120	Sequence 120, Appl
243	146.5	11.6	148	15	US-10-074-978A-216	Sequence 216, Appl	316	92	7.3	44	12	US-09-826-734-72	Sequence 72, Appl
244	146.5	11.6	200	12	US-09-968-415-5	Sequence 5, Appl	317	91.5	7.3	213	9	US-09-738-626-5143	Sequence 5143, Appl
245	145.5	11.6	200	14	US-10-180-719-5	Sequence 146, Appl	318	90.5	7.2	72	12	US-10-424-599-210705	Sequence 210705, A
246	145.5	11.4	213	15	US-10-004-378A-146	Sequence 7, Appl	319	89.5	7.1	38	9	US-09-879-792-18	Sequence 18, Appl
247	143.5	11.4	52	9	US-09-832-197-7	Sequence 7, Appl	320	88	7.0	30	9	US-09-820-893-111	Sequence 111, Appl
248	143.5	11.4	52	14	US-10-162-742-7	Sequence 7, Appl	321	88	7.0	48	9	US-09-910-151-8	Sequence 8, Appl
249	142.5	11.3	81	13	US-10-045-367A-7	Sequence 7, Appl	322	88	7.0	48	9	US-09-888-615-116	Sequence 116, Appl
250	142.5	11.3	81	14	US-10-170-789-57	Sequence 7, Appl	323	87	6.9	35	9	US-09-885-441-8	Sequence 8, Appl
251	142.5	11.3	130	15	US-10-291-265-714	Sequence 714, Appl	324	86.5	6.9	35	12	US-10-424-836-8	Sequence 8, Appl
252	138.5	11.0	49	14	US-10-029-386-1646	Sequence 1646, A	325	86.5	6.9	35	12	US-09-826-230-120	Sequence 120, Appl
253	136	10.8	196	9	US-09-764-898-134	Sequence 194, Appl	326	85.5	6.8	29	9	US-10-276-774-2659	Sequence 2659, A
254	136	10.8	196	9	US-09-764-898-267	Sequence 267, Appl	327	84.5	6.7	123	12	US-09-864-761-35323	Sequence 35323, A
255	135.5	10.8	146	10	US-09-925-297-643	Sequence 643, Appl	328	84	6.7	225	9	US-09-764-898-227	Sequence 227, Appl
256	135.5	10.8	156	12	US-10-424-599-149734	Sequence 149734, A	329	84	6.7	225	10	US-09-989-442-131	Sequence 131, Appl
257	133	10.6	146	9	US-09-864-408A-608	Sequence 608, Appl	330	84	6.7	225	16	US-10-297-987B-23	Sequence 23, Appl
258	131.5	10.5	78	11	US-10-029-386-29504	Sequence 29504, A	331	81.5	6.5	224	12	US-10-424-599-268213	Sequence 268213, A
259	131	10.4	79	14	US-10-029-386-31617	Sequence 31617, A	332	81.5	6.5	224	12	US-10-144-678A-1032	Sequence 1032, A
260	131	10.4	113	14	US-10-029-386-31617	Sequence 31617, A	333	81	6.4	15	14	US-10-294-025-1032	Sequence 1032, A
261	129	10.3	224	15	US-10-074-566-43	Sequence 43, Appl	334	81	6.4	15	14	US-10-045-170A-16	Sequence 16, Appl
262	128	10.2	189	15	US-10-074-566-66	Sequence 66, Appl	335	81	6.4	18	14	US-10-044-708A-29	Sequence 29, Appl
263	128	10.2	189	15	US-10-074-566-74	Sequence 74, Appl	336	81	6.4	18	14	US-09-826-230-247	Sequence 247, Appl
264	128	10.2	198	13	US-10-000-512-16	Sequence 16, Appl	337	80	6.4	18	16	US-10-264-309-68	Sequence 68, Appl
265	128	10.2	198	15	US-10-074-566-16	Sequence 16, Appl	338	80	6.4	18	16	US-09-820-893-110	Sequence 110, Appl
266	126.5	10.1	101	9	US-09-925-299-1243	Sequence 1243, A	339	80	6.4	30	12	US-10-607-565-110	Sequence 110, Appl
267	126.5	10.1	101	10	US-09-925-299-1243	Sequence 1243, A	340	80	6.4	30	12	US-10-297-987B-14	Sequence 14, Appl
268	125	9.9	166	9	US-09-925-299-1177	Sequence 1177, A	341	79	6.3	17	16	US-10-297-987B-13	Sequence 13, Appl
269	125	9.9	166	10	US-09-925-299-1177	Sequence 1177, A	342	79	6.3	18	16	US-10-128-965-36	Sequence 36, Appl
270	122.5	9.7	184	14	US-10-029-386-33844	Sequence 33844, A	343	79	6.3	27	14	US-09-779-323-1	Sequence 1, Appl
271	121	9.6	124	14	US-10-357-175-157	Sequence 157, Appl	344	78.5	6.2	188	9	US-10-071-214-12	Sequence 12, Appl
272	120	9.5	44	9	US-09-910-151-7	Sequence 7, Appl	345	78.5	6.2	31	12	US-10-071-214-12	Sequence 12, Appl
273	117	9.3	60	14	US-10-094-507-22	Sequence 22, Appl	346	77.5	6.2	23	9	US-09-879-792-22	Sequence 22, Appl
274	115	9.1	53	9	US-09-864-761-44996	Sequence 44996, A	347	77.5	6.2	159	15	US-10-108-260A-2919	Sequence 2919, A
275	115	9.1	118	15	US-10-104-047-3004	Sequence 3004, A	348	77	6.1	23	14	US-10-044-708A-30	Sequence 30, Appl
276	114.5	9.1	68	14	US-10-029-386-31171	Sequence 31171, A	349	76	6.0	26	14	US-10-128-965-25	Sequence 25, Appl
277	113.5	9.0	172	9	US-09-764-898-328	Sequence 328, A	350	76	6.0	31	12	US-10-071-214-13	Sequence 13, Appl
278	113	9.0	84	9	US-09-925-297-855	Sequence 855, A	351	76	6.0	156	12	US-10-424-599-213269	Sequence 213269, A
279	112	8.9	133	15	US-10-264-237-2660	Sequence 2660, A	352	75	6.0	29	12	US-10-253-286-374	Sequence 374, A
280	111	8.8	55	14	US-10-128-966-22	Sequence 22, Appl	353	75	6.0	29	15	US-10-245-871-374	Sequence 374, A
281	111	8.8	92	12	US-10-319-519-37	Sequence 37, Appl	354	75	6.0	50	14	US-10-128-965-42	Sequence 42, Appl
282	110.5	8.8	69	9	US-09-804-156-20	Sequence 20, Appl	355	74.5	5.9	82	10	US-09-903-463-16	Sequence 16, Appl
283	110.5	8.8	69	9	US-09-804-156-37	Sequence 37, Appl	356	74	5.9	23	12	US-10-071-214-6	Sequence 6, Appl
284	110.5	8.8	69	9	US-09-910-151-10	Sequence 10, Appl	357	74	5.9	23	12	US-10-071-214-7	Sequence 7, Appl
285	110.5	8.8	69	13	US-10-067-761-20	Sequence 20, Appl	358	74	5.9	23	12	US-10-071-214-8	Sequence 8, Appl
286	110.5	8.8	69	13	US-10-067-761-37	Sequence 37, Appl	359	74	5.9	42	16	US-10-297-987B-17	Sequence 17, Appl
287	110.5	8.8	69	14	US-10-319-519-20	Sequence 20, Appl	360	74	5.9	47	9	US-09-864-761-45041	Sequence 45041, A
288	110.5	8.8	69	14	US-10-319-519-37	Sequence 37, Appl	361	73.5	5.8	125	12	US-10-425-114-57102	Sequence 57102, A
289	110	8.7	98	9	US-09-910-151-11	Sequence 11, Appl	362	73	5.8	76	14	US-10-148-671-20	Sequence 20, Appl
290	108	8.6	57	9	US-09-864-761-43239	Sequence 43239, A	363	72	5.7	17	9	US-09-879-792-17	Sequence 17, Appl
291	108	8.6	85	12	US-09-826-734-222	Sequence 222, A	364	72	5.7	38	12	US-10-071-214-9	Sequence 9, Appl
292	107.5	8.5	194	9	US-09-764-898-285	Sequence 285, A	365	72	5.7	106	12	US-10-424-599-269407	Sequence 269407, A
293	106	8.4	66	12	US-09-826-734-76	Sequence 76, Appl	366	72	5.7	110	15	US-10-104-047-3008	Sequence 3008, A
294	106	8.4	138	11	US-09-864-408A-1486	Sequence 1486, A	367	71.5	5.7	114	12	US-10-424-599-232164	Sequence 232164, A
295	105.5	8.4	46	9	US-09-864-408A-5460	Sequence 5460, A	368	71	5.6	24	12	US-09-885-441-9	Sequence 9, Appl
296	104.5	8.3	46	9	US-09-888-615-117	Sequence 117, A	369	71	5.6	36	10	US-09-860-739-3	Sequence 3, Appl
297	103.5	8.2	62	12	US-10-424-599-218061	Sequence 218061, A	370	71	5.6	36	10	US-09-860-739-3	Sequence 3, Appl
298	102.5	8.1	200	9	US-09-925-300-1262	Sequence 1262, A	371	71	5.6	173	9	US-09-915-582-97	Sequence 97, Appl
299	101.5	8.1	37	9	US-09-864-761-34983	Sequence 34983, A	372	71	5.6	173	14	US-10-277-802-97	Sequence 97, Appl
300	101.5	8.1	42	9	US-09-885-41-7	Sequence 7, Appl	373	71	5.6	201	15	US-10-369-493-19553	Sequence 19553, A
301	101.5	8.1	42	12	US-10-424-836-7	Sequence 7, Appl	374	71	5.6	209	12	US-10-425-114-59509	Sequence 59509, A
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ALIGNMENTS

RESULT 1

US-10-072-012-611
 ; Publication 611, Application US/10072012
 ; Publication No. US20040033493A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Tchernev, Velizar
 ; APPLICANT: Spytek, Kimberly
 ; APPLICANT: Zerkhusen, Bryan
 ; APPLICANT: Fatturajan, Meera
 ; APPLICANT: Shamkets, Richard
 ; APPLICANT: Li, Li
 ; APPLICANT: Gangolli, Esha
 ; APPLICANT: Padigaru, Muralidhara
 ; APPLICANT: Anderson, David W.
 ; APPLICANT: Pastelli, Luca
 ; APPLICANT: Miller, Charles E.
 ; APPLICANT: Gerlach, Valerie
 ; APPLICANT: Taupier Jr, Raymond J.
 ; APPLICANT: Gusev, Vladimir Y.
 ; APPLICANT: Colman, Steven D.
 ; APPLICANT: Wolenc, Adam R.


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; APPLICANT: Pena, Carol E. A
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grosse, William M.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
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; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
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; US-10-072-012-611

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Best Local Similarity 53.1%; Pred. No. 3.5e-60;
Matches 120; Conservative 35; Mismatches 69; Indels 2; Gaps 2;

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RESULT 2
US-09-933-767-1150
; Sequence 1150, Application US/09933767
; Publication No. US20030181692A1
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; APPLICANT: Ni et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P2
; CURRENT APPLICATION NUMBER: US/09/933,767
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: PCT/US01/05614
; PRIOR FILING DATE: 2001-02-21
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; PRIOR FILING DATE: 1997-06-06
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; PRIOR APPLICATION NUMBER: 60/068,054
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; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/092,921
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: 60/094,657
; PRIOR FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1245
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; LENGTH: 228
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US-09-933-767-1150
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; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/10/004,860
; CURRENT FILING DATE: 2001-12-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 1150
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-004-860-1150

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; TITLE OF INVENTION: 207 Human Secreted Proteins
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; CURRENT FILING DATE: 2001-12-20
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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,998
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1150
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-023-282-1150
```

```

Query Match      51.7%; Score 651; DB 14; Length 228;
Best Local Similarity 91.7%; Pred. No. 2,4e-57;
Matches 121; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 1 IIKGFECKPHSQPQWQAALFEKTRLLCGATLIAPRWLLTAACHLKPRYIVHLGQHNLOKEE 60
Db 4 IIKGFECKLHSPQWQAALFEKTRLLCGATLIAPRWLLTAACHLKPRYIVHLGQHNLOKEE 63
QY 61 GCEQRTATESPPHGFNNSLPNKDHRNDIMLVKVASPVSIWAVRPLTSSRCVTAGTS 120
Db 64 GCEQRTATESPPHGFNNSLPNKDHRNDIMLVKVASPVSIWAVRPLTSSRCVTAGTS 123
QY 121 CLISWGSTSSP 132
Db 124 CSFPAGAAARPDP 135
```

```

RESULT 5
US-09-739-907-180
; Sequence 180, Application US/09739907
; Patent No. US20010012889A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
```

```

; TITLE OF INVENTION: 36 Human Secreted Proteins
; FILE REFERENCE: P2022P1
; CURRENT APPLICATION NUMBER: US/09/739,907
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 09/348,457
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: 60/070,567
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: 60/070,692
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: 60/070,704
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: 60/070,658
; PRIOR FILING DATE: 1998-01-07
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 180
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-739-907-180
```

```

Query Match      50.1%; Score 630.5; DB 9; Length 220;
Best Local Similarity 50.7%; Pred. No. 2.7e-55;
Matches 114; Conservative 39; Mismatches 65; Indels 7; Gaps 4;

QY 7 CKPHSQPQWQAALFEKTRLLCGATLIAPRWLLTAACHLKPRYIVHLGQHNLOK-EEGCEQ 64
Db 1 CDHMTQWQAALLLRPNQLYCGAVLVHPQWLLTAACHCKKVRVRLGHVLSLPYVESGQQ 60
QY 65 TRTATESPPHGFNNSLPNKDHRNDIMLVKVASPVSIWAVRPLTSSRCVTAGTSCLIS 124
Db 61 MFCQVKSIPIHFGYS----HFGHNDLMLIKLNRRIPTKDVRFINVSCHSPSAGTKCLVS 116
QY 125 GWGSTSPQLRLPHTLRCANITIEHOKCENAYPGNITDMVCASVQEGGKDCQGDSSG 184
Db 117 GWGTTKSPQVHPKVLQCLNISVLSQKCEDAIPRQIDDTMFAG-DKAGRDSQGDSSG 175
QY 185 PLVNCNLSQGLIISWGQDPCAITRKPGYIVTKYKVDWIQETMRKN 229
Db 176 PIVCNGSLQGLVSWGDPYPCARPNNRGYVITNLCKFTKWIQETIQAN 220
```

```

RESULT 6
US-09-938-671-180
; Sequence 180, Application US/09938671
; Publication No. US20040002066A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 36 Human Secreted Proteins
; FILE REFERENCE: P2022P1
; CURRENT APPLICATION NUMBER: US/09/938,671
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: 09/348,457
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: 60/070,567
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: 60/070,692
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: 60/070,704
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: 60/070,658
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 180
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-938-671-180
```

```

Query Match      50.1%; Score 630.5; DB 11; Length 220;
Best Local Similarity 50.7%; Pred. No. 2.7e-55;
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Matches	114;	Conservative	39;	Mismatches	65;	Indels	7;	Gaps	4;
QY	7	CKPISQWQAA-LPEKTRLLCCGATLAPRWLLTAAHCLKPRYIVHGLQHNLQK-EEGCEQ	64						
Db	1	CDMHTQWQAALLRPNQLYCGAVLHPQWLLTAAHCKKVFRLGHVSLSPVYESQQ	60						
QY	65	TRTATESPPHGFNNSLPNKDHNDMLVOMASPVSIITWAVRPLTSLERCVTAGTSCLS	124						
Db	61	MFQVKSIPIPHGYS- ---HPGSHNDLMLKLNRIIRPTKDVPRPINVSSHCP-SAGTKCLVS	116						
QY	125	GWGSTSSPOLRLPHTLRSCANITIEHQKCNENAYPGNITDTWVCASVQEGGKDSQCGDSGG	184						
Db	117	GWGITKSPQVHFPPKVQCLMISVLVSQKRCEDAIAPROIDITNFCAG-DRAGRDSQCGDSGG	175						
QY	185	PLVNCNSLQGIISWGQDPFCALTREKPGYTKVKCYVDWIQIETMKN	229						
Db	176	PWVNGSIFOGIIVSGNDYPCARPNNRPGYTNLCFTKWIQETIOAN	220						

RESULT 7
 US-10-654-823-2
 ; Sequence 2, Application US/10654823
 ; Publication No. US20040049812A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Howard, John A.
 ; APPLICANT: Hood, Elizabeth
 ; TITLE OF INVENTION: COMMERCIAL PRODUCTION OF PROTEASES IN PLANTS
 ; FILE REFERENCE: 10014
 ; CURRENT APPLICATION NUMBER: US/10/654,823
 ; CURRENT FILING DATE: 2003-09-04
 ; PRIOR APPLICATION NUMBER: US/09/120,582
 ; PRIOR FILING DATE: 1998-07-22
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 229
 ; TYPE: PRT
 ; ORGANISM: Bos taurus
 ; US-10-654-823-2

RESULT 8
US-09-910-071-14
; Sequence 14, Application US/09910071
; Patent No. US20020116146A1
; GENERAL INFORMATION:
; APPLICANT: Tonikawa, Mayumi
; APPLICANT: Aikawa, Seiichi
; APPLICANT: Matsuzawa, Fumiko
; TITLE OF INVENTION: Method and Apparatus for Extracting and Evaluating Mutually Similar
; TITLE OF INVENTION: Portions in One-Dimensional Sequences in Molecules and/or Three-
; TITLE OF INVENTION: Structures of Molecules
; FILE REFERENCE: 522.1921D2

```

; CURRENT APPLICATION NUMBER: US/09/910,071
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 08/014,867
; PRIOR FILING DATE: 1993-02-08
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 223
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: amino acid sequence of trypsin
US-09-910-071-14

Query Match      44.8%; Score 563; DB 9; Length 223;
Best Local Similarity 46.7%; Pred. No. 1.8e-48;
Matches 107; Conservative 38; Mismatches 78; Indels 6; Gaps 3;

QY      1 I I K G P E C K P S Q F W Q A A L F E K T R L L C G A T L I A P R M L L T A A H C L K P R Y I V H L G H N L Q K E E 60
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1 I V G Y T C C A N T P V Y Q V S L - N S G Y H F C G S L I N S Q W Y V S A A H C Y K S G I Q V R L G E D N I N V Y E 59

QY      61 G C E Q T E T A T E S P H P G F N N S L P N K D H R N D I M L V K M A S P V S I T W A V R P L T L S R C V T A G T S 120
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      60 G N E Q F I S A K S I V H P S Y N S T L N - - - N D I M L I K L S A A S L N S R V A S I S L P T S C A S A G T Q 115

QY      121 C L I S G W G T S S P Q L R L P H T L R C A N T I I E H Q C E N A Y P G N I T D T W V C A S V O E G G K D S C O G 180
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      116 C L I S G M G N T K S G T S Y P D Y L K L K A P I L S D S S C K S A Y P G Q I T S N M F C A G Y L E G G K D S C O G 175

QY      181 D S G G P L V C N Q S L Q G I I S W Q D D F C A I T R K E G V T K V C Y V D W I Q E T M K N N 229
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      176 D S G G P W C S G K L G I V S W G S G - C A C N K P E V T K V G N Y S W I T K Q T I A S N 223

```

RESULT 9
US-09-898-837A-50
Sequence 50, Application US/09898837A
Publication No. US20030077697A1
GENERAL INFORMATION:
APPLICANT: Quinn, Kerry E.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Majumder, Komud
APPLICANT: Vermet, Corine
APPLICANT: Herzmann, John L.
APPLICANT: Burgess, Catherine
APPLICANT: Fernandes, Elma
APPLICANT: Taupier Jr., Raymond
APPLICANT: Rastelli, Luca
APPLICANT: Curagen Corporation
APPLICANT: Gerlach, Valerie L
APPLICANT: MacDougall, John R
TITLE OF INVENTION: NOVEL SERINE/THREONINE PROTEIN-KINASE LIKE PROTEINS AND
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING THE SAME
FILE REFERENCE: 15966-598 CIP
CURRENT APPLICATION NUMBER: US/09/898,837A
CURRENT FILING DATE: 2001-07-03
PRIOR APPLICATION NUMBER: U.S.S.N. 60/165,986
PRIOR FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: U.S.S.N. 60/194,839
PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: U.S.S.N. 60/195,637
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: U.S.S.N. 60/197,080
PRIOR FILING DATE: 2000-04-13
PRIOR APPLICATION NUMBER: U.S.S.N. 60/232,677
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: U.S.S.N. 60/181,347
PRIOR FILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: U.S.S.N. 60/194,195
PRIOR FILING DATE: 2000-04-03
PRIOR APPLICATION NUMBER: U.S.S.N. 60/215,906
PRIOR FILING DATE: 2000-07-03

	Query Match	43.4%	Score 546;	DB 16;	Length 225;
	Best Local Similarity	43.7%;	Pred. No. 9.4e-47;		
	Matches 100;	Conservative 37;	Mismatches 86;	Indels	Gaps 2;
QY	1	IIKFECKPHSQPQAALPEKFTALLCGATLLIAPRWLLTAHCLKPRYIVHLCQHNMQKEE	60		
Db	2	IIDGAPCARGHPQVALLSGNQLHCGVLVNERWVLTAAHCKMNEYTVHLSGDTLGDRR	61		
QY	61	GCEQTRTATESFPHPGNNSLPNKDRNDIMLVKMAPSVITWAVRPTLTLSRCVCVTAQTS	120		
Db	62	A--GRKASKSFRHPGYS---TQTHVNDLMLVKLASQARLSSWMVKVRLPSRCEPPTT	115		
QY	121	CLISGWGSTSPQLRPHLTRCANITIIHCKENAYPGNITDTWVCASVEGKHSCQG	180		
Db	116	CTVSGWGTSTSDVTFESDLMCVDDVKLISPDQCTKYVKDLENSMLCAGIPDSKKNACNG	175		

```

RESULT 12
US-10-312-089-8
; Sequence 8, Application US/10312089
; Publication No. US20030143240A1
; GENERAL INFORMATION:
; APPLICANT: Cabazon-Silva, Teresa Elisa Virginia
; APPLICANT: Perranne, Philippe Jean gervais Ghislain
; TITLE OF INVENTION: Prostate Protein Vaccine Comprising
; TITLE OF INVENTION: Derivatised Thiol Residues and Methods for Producing Said
; TITLE OF INVENTION: Antigen
; FILE REFERENCE: B45224
; CURRENT APPLICATION NUMBER: US/10/312,089
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: PCT/EP01/07082
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: GB 0015722.2
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0

```

SEQ ID NO 8
 LENGTH: 226
 TYPE: PRT
 ORGANISM: Homo sapien
 US-10-312-089-8

Query Match 41.6%; Score 523.5; DB 14; Length 226;
 Best Local Similarity 42.2%; Pred. No. 1.8e-44;
 Matches 95; Conservative 47; Mismatches 76; Indels 7; Gaps 3;

QY 4 GFCEKPSQWQAALFEKTRLLCGATLIAPRWLLTAACHLKPRYIVHLGQHNLO-KEEGC 62
 DB 6 GEDCSPHSQWQAALVMESELFCSGVLVHPQWLSAAHCFQNSYITIGLHLSLEADQEPG 65
 QY 63 BQRTATESPFPFGFNNSLPNKDRNDIMLVKASPVISITWAVRPLTLSSRCVTAGTSC 122
 DB 66 SOWEASLSVRHPEYRPL----LANDMLIKLDESSESSTIRSISIAOCPAGNSCL 121
 QY 123 ISGWSTSSPOLRPLPHTLRCAITIEHOKCENAYPGNITDTMVCASVQEGGKDCSQGDS 182
 DB 122 VSGWLLANG--RMTVLQCVNVSVSEVCSKLYDPLVHPSMFCAGGQDQKDCSNGDS 179
 QY 183 GGPLVNCQSLQGIISWGQDPCATRKPGVYTKVCKYVDWIQETMK 227
 DB 180 GGPLICNGYLQGLVSPGKAPCGQGVGVYTNLCCKFTWIEKTVQ 224

RESULT 13

US-09-759-143-327
 Sequence 327, Application US/09759143
 Patent No. US2002022248A1
 GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
 APPLICANT: Dillon, Davin C.
 APPLICANT: Mitcham, Jennifer L.
 APPLICANT: Harlocker, Susan L.
 APPLICANT: Jiang, Yuqi
 APPLICANT: Henderson, Robert A.
 APPLICANT: Kalos, Michael D.
 APPLICANT: Fanger, Gary R.
 APPLICANT: Retter, Marc W.
 APPLICANT: Stolk, John A.
 APPLICANT: Day, Craig H.
 APPLICANT: Vedvick, Thomas S.
 APPLICANT: Carter, Darrick
 APPLICANT: Li, Samuel
 APPLICANT: Wang, Aijun
 APPLICANT: Skeiky, Yasir A.W.
 APPLICANT: Hepler, William

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
 FILE REFERENCE: 210121.427C23
 CURRENT APPLICATION NUMBER: US/09/759,143
 CURRENT FILING DATE: 2001-01-12
 NUMBER OF SEQ ID NOS: 934

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 327
 LENGTH: 220
 TYPE: PRT

ORGANISM: Homo sapien
 US-09-759-143-327

Query Match 41.4%; Score 520.5; DB 9; Length 220;
 Best Local Similarity 42.2%; Pred. No. 3.4e-44;
 Matches 94; Conservative 47; Mismatches 75; Indels 7; Gaps 3;

QY 6 ECKPHSQWQAALFEKTRLLCGATLIAPRWLLTAACHLKPRYIVHLGQHNLO-KEEGC 64
 DB 2 DCSPHSQWQAALVMESELFCSGVLVHPQWLSAAHCFQNSYITIGLHLSLEADQEPG 61
 QY 65 TRTATESPFPFGFNNSLPNKDRNDIMLVKASPVISITWAVRPLTLSSRCVTAGTSC 124
 DB 62 NVEASLSVRHPEYRPL----LANDMLIKLDESSESSTIRSISIAOCPAGNSCL 117

QY 125 GWGSTSSPOLRPLPHTLRCAITIEHOKCENAYPGNITDTMVCASVQEGGKDCSQGDSG 184
 DB 118 GWGLLANG--RMTVLQCVNVSVSEVCSKLYDPLVHPSMFCAGGQDQKDCSNGDSG 175
 QY 185 PLVNCQSLQGIISWGQDPCATRKPGVYTKVCKYVDWIQETMK 227
 DB 176 PLICNGYLQGLVSPGKAPCGQGVGVYTNLCCKFTWIEKTVQ 218

RESULT 14

US-09-780-669-327
 Sequence 327, Application US/09780669
 Patent No. US20020051977A1
 GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
 APPLICANT: Dillon, Davin C.
 APPLICANT: Mitcham, Jennifer L.
 APPLICANT: Harlocker, Susan L.
 APPLICANT: Jiang, Yuqi
 APPLICANT: Henderson, Robert A.
 APPLICANT: Kalos, Michael D.
 APPLICANT: Fanger, Gary R.
 APPLICANT: Retter, Marc W.
 APPLICANT: Stolk, John A.
 APPLICANT: Day, Craig H.
 APPLICANT: Vedvick, Thomas S.
 APPLICANT: Carter, Darrick
 APPLICANT: Li, Samuel
 APPLICANT: Wang, Aijun
 APPLICANT: Skeiky, Yasir A.W.
 APPLICANT: Hepler, William
 APPLICANT: McNeill, Patricia D.
 APPLICANT: Houghton, Raymond L.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
 FILE REFERENCE: 210121.427C24
 CURRENT APPLICATION NUMBER: US/09/780,669
 CURRENT FILING DATE: 2001-02-09
 NUMBER OF SEQ ID NOS: 943

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 327
 LENGTH: 220
 TYPE: PRT

ORGANISM: Homo sapien
 US-09-780-669-327

Query Match 41.4%; Score 520.5; DB 9; Length 220;
 Best Local Similarity 42.2%; Pred. No. 3.4e-44;
 Matches 94; Conservative 47; Mismatches 75; Indels 7; Gaps 3;

QY 6 ECKPHSQWQAALFEKTRLLCGATLIAPRWLLTAACHLKPRYIVHLGQHNLO-KEEGC 64
 DB 2 DCSPHSQWQAALVMESELFCSGVLVHPQWLSAAHCFQNSYITIGLHLSLEADQEPG 61
 QY 65 TRTATESPFPFGFNNSLPNKDRNDIMLVKASPVISITWAVRPLTLSSRCVTAGTSC 124
 DB 62 NVEASLSVRHPEYRPL----LANDMLIKLDESSESSTIRSISIAOCPAGNSCL 117
 QY 125 GWGSTSSPOLRPLPHTLRCAITIEHOKCENAYPGNITDTMVCASVQEGGKDCSQGDSG 184
 DB 118 GWGLLANG--RMTVLQCVNVSVSEVCSKLYDPLVHPSMFCAGGQDQKDCSNGDSG 175
 QY 185 PLVNCQSLQGIISWGQDPCATRKPGVYTKVCKYVDWIQETMK 227
 DB 176 PLICNGYLQGLVSPGKAPCGQGVGVYTNLCCKFTWIEKTVQ 218

RESULT 15

US-09-822-827-327
 Sequence 327, Application US/09822827
 Patent No. US20020081680A1

GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.534C1
CURRENT APPLICATION NUMBER: US/09/822,827
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 327
LENGTH: 220
TYPE: PRT
ORGANISM: Homo sapien
US-09-822-827-327

Query Match 41.4%; Score 520.5; DB 9; Length 220;
Best Local Similarity 42.2%; Pred. No. 3.4e-44;
Matches 94; Conservative 47; Mismatches 75; Indels 7; Gaps 3;
QY 6 ECKPHSQWQAALFEKTRLLCGATLIAPRWLLTAACHLKPRYIVHLGQHNLO-KEEGCEQ 64
DB 2 DCSPHSQWQAALVWENELFCGVLVHPQWVLSAAHCFQNSYITGLHLSLEADQEPGSQ 61
QY 65 TTTATESFPHPGNNPLPKNDHNDIMLVKMASPVSIWAVRPLTLSSRCVYTAGTSCLS 124
DB 62 MVEASLSVRHPEYNRPL----LANDMLIKLDESVSSEDTIRSIASQCTAGNSCLVS 117
QY 125 GWGSTSSPOLRPLPHTLRCAITIEHOKCENAYPGNITDTMYCASVQEGGKDCSGDGG 184
DB 118 GWGLLANG--RMPVTLQCVNVSVSEVCSKLYDPLVHPSMFCAGGGQDQKDCSNGDSGG 175
QY 185 PLVCNOSLOGIISWGDPQCAITRKPGVYTKVKYVDWIQETMK 227
DB 176 PLICNGYLQGLVSGFKAPCGQGVPGVYTNLCKFTIEWIEKTQ 218

RESULT 16
US-09-232-880-327
Sequence 327, Application US/09232880
Publication No. US20020182596A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF
FILE REFERENCE: 210121.428C6
CURRENT APPLICATION NUMBER: US/09/232,880
CURRENT FILING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 338
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 327
LENGTH: 220
TYPE: PRT
ORGANISM: Homo sapien
US-09-232-880-327

Query Match 41.4%; Score 520.5; DB 9; Length 220;
Best Local Similarity 42.2%; Pred. No. 3.4e-44;
Matches 94; Conservative 47; Mismatches 75; Indels 7; Gaps 3;
QY 6 ECKPHSQWQAALFEKTRLLCGATLIAPRWLLTAACHLKPRYIVHLGQHNLO-KEEGCEQ 64
DB 2 DCSPHSQWQAALVWENELFCGVLVHPQWVLSAAHCFQNSYITGLHLSLEADQEPGSQ 61
QY 65 TTTATESFPHPGNNPLPKNDHNDIMLVKMASPVSIWAVRPLTLSSRCVYTAGTSCLS 124
DB 62 MVEASLSVRHPEYNRPL----LANDMLIKLDESVSSEDTIRSIASQCTAGNSCLVS 117
QY 125 GWGSTSSPOLRPLPHTLRCAITIEHOKCENAYPGNITDTMYCASVQEGGKDCSGDGG 184
DB 118 GWGLLANG--RMPVTLQCVNVSVSEVCSKLYDPLVHPSMFCAGGGQDQKDCSNGDSGG 175

QY 185 PLVCNOSLOGIISWGDPQCAITRKPGVYTKVKYVDWIQETMK 227
DB 176 PLICNGYLQGLVSGFKAPCGQGVPGVYTNLCKFTIEWIEKTQ 218
RESULT 17
US-09-895-793-327
Sequence 327, Application US/09895793
Publication No. US20020192763A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.534C2
CURRENT APPLICATION NUMBER: US/09/895,793
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 327
LENGTH: 220
TYPE: PRT
ORGANISM: Homo sapien
US-09-895-793-327

Query Match 41.4%; Score 520.5; DB 9; Length 220;
Best Local Similarity 42.2%; Pred. No. 3.4e-44;
Matches 94; Conservative 47; Mismatches 75; Indels 7; Gaps 3;
QY 6 ECKPHSQWQAALFEKTRLLCGATLIAPRWLLTAACHLKPRYIVHLGQHNLO-KEEGCEQ 64
DB 2 DCSPHSQWQAALVWENELFCGVLVHPQWVLSAAHCFQNSYITGLHLSLEADQEPGSQ 61
QY 65 TTTATESFPHPGNNPLPKNDHNDIMLVKMASPVSIWAVRPLTLSSRCVYTAGTSCLS 124
DB 62 MVEASLSVRHPEYNRPL----LANDMLIKLDESVSSEDTIRSIASQCTAGNSCLVS 117
QY 125 GWGSTSSPOLRPLPHTLRCAITIEHOKCENAYPGNITDTMYCASVQEGGKDCSGDGG 184
DB 118 GWGLLANG--RMPVTLQCVNVSVSEVCSKLYDPLVHPSMFCAGGGQDQKDCSNGDSGG 175
QY 185 PLVCNOSLOGIISWGDPQCAITRKPGVYTKVKYVDWIQETMK 227
DB 176 PLICNGYLQGLVSGFKAPCGQGVPGVYTNLCKFTIEWIEKTQ 218

RESULT 18
US-09-895-814-327
Sequence 327, Application US/09895814
Publication No. US20020193296A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.


```

; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Wantanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 327
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-895-814-327

Query Match 41.4%; Score 520.5; DB 9; Length 220;
Best Local Similarity 42.2%; Pred. No. 3.4e-44;
Matches 94; Conservative 47; Mismatches 75; Indels 7; Gaps 3;

QY 6 ECKPHSQPQAAALFEKTRLLCGATLIAPRWLLTAACHLKPRYIVHLGQHNLO-KEEGCEQ 64
DB 2 DCSPHSQPQAAALVWENELFCGVLVHPQVLSAHCQFNSYITGLGLHSLEADQEPGSG 61
QY 65 TRTATESPFPHPGNNSLPNKDHRNDIMLVKMASPVISITWAVRPLTLSSRCVTAAGTSCGIS 124
DB 62 MVEASLSVRHPEYNRPL----LANDLMLIKLDESVSSESDTIRSIASQCPAGNSCLVS 117
QY 125 GWGSTSPQLRPLHTLRCAITIEHOKCENAYPGNITDTMVCASVQEGGKDCSGDGG 184
DB 118 GWGLLANG--RMPTVLQCVNVSVSEVCSKLYDPLVHPNMFACAGGQDQKDCSGDGG 175
QY 185 PLVCNOSLQIISWGQDPCAITRKPGVYTKVKYVDWMIQETMK 227
DB 176 PLICNGYLQGLVSGKAPCGQGVGVYTNLCKFTEWIEKTQV 218

RESULT 19
US-10-012-896-327
; Sequence 327, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.

```

```

; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Wantanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 327
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-012-896-327

Query Match 41.4%; Score 520.5; DB 13; Length 220;
Best Local Similarity 42.2%; Pred. No. 3.4e-44;
Matches 94; Conservative 47; Mismatches 75; Indels 7; Gaps 3;

QY 6 ECKPHSQPQAAALFEKTRLLCGATLIAPRWLLTAACHLKPRYIVHLGQHNLO-KEEGCEQ 64
DB 2 DCSPHSQPQAAALVWENELFCGVLVHPQVLSAHCQFNSYITGLGLHSLEADQEPGSG 61
QY 65 TRTATESPFPHPGNNSLPNKDHRNDIMLVKMASPVISITWAVRPLTLSSRCVTAAGTSCGIS 124
DB 62 MVEASLSVRHPEYNRPL----LANDLMLIKLDESVSSESDTIRSIASQCPAGNSCLVS 117
QY 125 GWGSTSPQLRPLHTLRCAITIEHOKCENAYPGNITDTMVCASVQEGGKDCSGDGG 184
DB 118 GWGLLANG--RMPTVLQCVNVSVSEVCSKLYDPLVHPNMFACAGGQDQKDCSGDGG 175
QY 185 PLVCNOSLQIISWGQDPCAITRKPGVYTKVKYVDWMIQETMK 227
DB 176 PLICNGYLQGLVSGKAPCGQGVGVYTNLCKFTEWIEKTQV 218

RESULT 20
US-10-010-940-327
; Sequence 327, Application US/10010940
; Publication No. US20030088062A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqiu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427D3
; CURRENT APPLICATION NUMBER: US/10/010,940
; CURRENT FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 327
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-010-940-327

```

```
Query Match 41.4%; Score 520.5; DB 14; Length 220;
Best Local Similarity 42.2%; Pred. No. 3.4e-44;
Matches 94; Conservative 47; Mismatches 75; Indels 7; Gaps 3;

QY 6 ECKPHSQWQAALFEKTRLLCGATLIAPRWLLTAACHLKPRYIVHLGQHNLO-KEEGCEQ 64
Db 2 DCSPHSQWQAALVMENELFCSGVLVHPQWVLSAAHCFQNSYITIGLHLSLEADQEPGSG 61
QY 65 TRTATESFPHGPNNSLPNKDHRNDIMLVKASPVSIITWAVRPLTSSRCVITAGTSCGIS 124
Db 62 MVEASLSVRHPEYNRPL----LANDMLIKLDESVSSEDTRISIASQCPTAGNSCLVS 117
QY 125 GWGSTSSPOLRLPHTLRCAITIIHOKCENAYPGNITDTMVCASVQEGGKDCSGDGG 184
Db 118 GWGLLANG--RMTVLQCVNVSVSEVCSKLYDPLHYHPSMFCAGGQDQKDCNGDGG 175
QY 185 PLVCNQSLOGIISWGQDPCCAITRKPGVYTKVCKYVDWIQETMK 227
Db 176 PLICNGYLQGLVSGKAPCGQGVGVYTNLCFTWIEKTVQ 218

RESULT 21
US-10-144-678A-327
; Sequence 327, Application US/10144678A
; Publication No. US20030157089A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Hepler, William T.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals y de Bassols, Carlota
; APPLICANT: Foy, Teresa M.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Deng, Ta
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C28
; CURRENT APPLICATION NUMBER: US/10/144,678A
; NUMBER OF SEQ ID NOS: 1033
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 327
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-144-678A-327

Query Match 41.4%; Score 520.5; DB 14; Length 220;
Best Local Similarity 42.2%; Pred. No. 3.4e-44;
Matches 94; Conservative 47; Mismatches 75; Indels 7; Gaps 3;

QY 6 ECKPHSQWQAALFEKTRLLCGATLIAPRWLLTAACHLKPRYIVHLGQHNLO-KEEGCEQ 64
Db 2 DCSPHSQWQAALVMENELFCSGVLVHPQWVLSAAHCFQNSYITIGLHLSLEADQEPGSG 61
QY 65 TRTATESFPHGPNNSLPNKDHRNDIMLVKASPVSIITWAVRPLTSSRCVITAGTSCGIS 124
Db 62 MVEASLSVRHPEYNRPL----LANDMLIKLDESVSSEDTRISIASQCPTAGNSCLVS 117
QY 125 GWGSTSSPOLRLPHTLRCAITIIHOKCENAYPGNITDTMVCASVQEGGKDCSGDGG 184
Db 118 GWGLLANG--RMTVLQCVNVSVSEVCSKLYDPLHYHPSMFCAGGQDQKDCNGDGG 175
QY 185 PLVCNQSLOGIISWGQDPCCAITRKPGVYTKVCKYVDWIQETMK 227
Db 176 PLICNGYLQGLVSGKAPCGQGVGVYTNLCFTWIEKTVQ 218

RESULT 22
US-10-294-025-327
; Sequence 327, Application US/10294025
; Publication No. US20030185830A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C29
; CURRENT APPLICATION NUMBER: US/10/294,025
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 1038
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 327
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-294-025-327

Query Match 41.4%; Score 520.5; DB 14; Length 220;
Best Local Similarity 42.2%; Pred. No. 3.4e-44;
Matches 94; Conservative 47; Mismatches 75; Indels 7; Gaps 3;

QY 6 ECKPHSQWQAALFEKTRLLCGATLIAPRWLLTAACHLKPRYIVHLGQHNLO-KEEGCEQ 64
Db 2 DCSPHSQWQAALVMENELFCSGVLVHPQWVLSAAHCFQNSYITIGLHLSLEADQEPGSG 61
QY 65 TRTATESFPHGPNNSLPNKDHRNDIMLVKASPVSIITWAVRPLTSSRCVITAGTSCGIS 124
Db 62 MVEASLSVRHPEYNRPL----LANDMLIKLDESVSSEDTRISIASQCPTAGNSCLVS 117
QY 125 GWGSTSSPOLRLPHTLRCAITIIHOKCENAYPGNITDTMVCASVQEGGKDCSGDGG 184
Db 118 GWGLLANG--RMTVLQCVNVSVSEVCSKLYDPLHYHPSMFCAGGQDQKDCNGDGG 175
QY 185 PLVCNQSLOGIISWGQDPCCAITRKPGVYTKVCKYVDWIQETMK 227
Db 176 PLICNGYLQGLVSGKAPCGQGVGVYTNLCFTWIEKTVQ 218

RESULT 23
US-10-051-874-101
; Sequence 101, Application US/10051874
; Publication No. US2004000557A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Alsobrook II, John P
; APPLICANT: Colman, Steven D
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Boldog, Ferenc
; APPLICANT: Vernet, Corine AM
; APPLICANT: Li, Li
; APPLICANT: Shenoy, Suresh J
; APPLICANT: Casman, Stacie J
; APPLICANT: Guo, Xiaojia Sasha
; APPLICANT: Edinger, Shlomit R
; APPLICANT: MacDougall, John R
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard A
```

```
Db 62 MVEASLSVRHPEYNRPL----LANDMLIKLDESVSSEDTRISIASQCPTAGNSCLVS 117
QY 125 GWGSTSSPOLRLPHTLRCAITIIHOKCENAYPGNITDTMVCASVQEGGKDCSGDGG 184
Db 118 GWGLLANG--RMTVLQCVNVSVSEVCSKLYDPLHYHPSMFCAGGQDQKDCNGDGG 175
QY 185 PLVCNQSLOGIISWGQDPCCAITRKPGVYTKVCKYVDWIQETMK 227
Db 176 PLICNGYLQGLVSGKAPCGQGVGVYTNLCFTWIEKTVQ 218

RESULT 22
US-10-294-025-327
; Sequence 327, Application US/10294025
; Publication No. US20030185830A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C29
; CURRENT APPLICATION NUMBER: US/10/294,025
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 1038
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 327
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-294-025-327

Query Match 41.4%; Score 520.5; DB 14; Length 220;
Best Local Similarity 42.2%; Pred. No. 3.4e-44;
Matches 94; Conservative 47; Mismatches 75; Indels 7; Gaps 3;

QY 6 ECKPHSQWQAALFEKTRLLCGATLIAPRWLLTAACHLKPRYIVHLGQHNLO-KEEGCEQ 64
Db 2 DCSPHSQWQAALVMENELFCSGVLVHPQWVLSAAHCFQNSYITIGLHLSLEADQEPGSG 61
QY 65 TRTATESFPHGPNNSLPNKDHRNDIMLVKASPVSIITWAVRPLTSSRCVITAGTSCGIS 124
Db 62 MVEASLSVRHPEYNRPL----LANDMLIKLDESVSSEDTRISIASQCPTAGNSCLVS 117
QY 125 GWGSTSSPOLRLPHTLRCAITIIHOKCENAYPGNITDTMVCASVQEGGKDCSGDGG 184
Db 118 GWGLLANG--RMTVLQCVNVSVSEVCSKLYDPLHYHPSMFCAGGQDQKDCNGDGG 175
QY 185 PLVCNQSLOGIISWGQDPCCAITRKPGVYTKVCKYVDWIQETMK 227
Db 176 PLICNGYLQGLVSGKAPCGQGVGVYTNLCFTWIEKTVQ 218

RESULT 23
US-10-051-874-101
; Sequence 101, Application US/10051874
; Publication No. US2004000557A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Alsobrook II, John P
; APPLICANT: Colman, Steven D
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Boldog, Ferenc
; APPLICANT: Vernet, Corine AM
; APPLICANT: Li, Li
; APPLICANT: Shenoy, Suresh J
; APPLICANT: Casman, Stacie J
; APPLICANT: Guo, Xiaojia Sasha
; APPLICANT: Edinger, Shlomit R
; APPLICANT: MacDougall, John R
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard A
```

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; APPLICANT: Pena, Carol EA
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Millet, Isabelle
; APPLICANT: Miller, Charles E
; APPLICANT: Lepley, Denise M
; APPLICANT: Smithson, Glenda
; APPLICANT: Baumgartner, Jason C
; APPLICANT: Herrman, John L
; APPLICANT: Peyman, John A
; APPLICANT: Gorman, Linda
; APPLICANT: Mezes, Peter D
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Gerlach, Valerie
; APPLICANT: Grosse, William M
; APPLICANT: Liu, Xiaohong
; APPLICANT: Ellerman, Karen
; APPLICANT: Rothenberg, Mark
; APPLICANT: Stone, David J
; APPLICANT: Burgess, Catherine E
; TITLE OF INVENTION: PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS OF
; TITLE OF INVENTION: USING THE SAME
; FILE REFERENCE: 21402-245
; CURRENT APPLICATION NUMBER: US/10/051,874
; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: 60/268,595
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/325,306
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 60/262,587
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: 60/272,409
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/262,454
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: 60/276,777
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/291,672
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/330,336
; PRIOR FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 60/265,530
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/261,376
; PRIOR FILING DATE: 2001-01-16
; NUMBER OF SEQ ID NOS: 269
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 101
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Tryp Spc,
; OTHER INFORMATION: Trypsin-like serine protease domain sequence
US-10-051-874-101

Query Match 40.3%; Score 507.5; DB 15; Length 229;
Best Local Similarity 47.4%; Pred. No. 7.4e-43;
Matches 111; Conservative 30; Mismatches 76; Indels 17; Gaps 8;

Qy 1 IIKGFECKPHSQPQWQAALFEK--TRLLCGATLIAPRWLLTAHCL---KPRYIVHLGQHN 55
Db 1 IVGSEANIGSFPMQVSLQYRGHFCGSLISPRWVLTAAHCVGSGAPSSIRVRLGSHD 60
Qy 56 LQKEEGCEQRTATSPHFGFNNSLPNKDHRNDIMLVKMASPVSTIWAVRPLTL--SSR 113
Db 61 LSSGEE--TQTVKSKVIVHNPYNS-----TYDNDIALLLKLEPEVTLSDTVRPICLPSSGY 115
Qy 114 CVTAGTCLISGWSGTSPPQLRPHLTRCANITIEHOKCENAYPGN--ITDTMVCASVQ 171
Db 116 NVPAGTCTVSGWGTSESSGSLPDTLQEVNPIVSNATCERAYSGGAIIDNMLCAGGL 175

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; APPLICANT: Curagen Corporation
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Fernandes, Elma R
; APPLICANT: Taupier, Raymond J
; APPLICANT: Quinn, Kerry E
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Rastelli, Luca
; APPLICANT: Herrman, John L
; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-750
; CURRENT APPLICATION NUMBER: US/09/825,751A
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 60/194,314
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: 60/225,693
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 72
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Consensus
; OTHER INFORMATION: Sequence
US-09-825-751A-72

Query Match 40.3%; Score 507; DB 12; Length 229;
Best Local Similarity 47.2%; Pred. No. 8.3e-43;
Matches 110; Conservative 30; Mismatches 77; Indels 16; Gaps 7;

Qy 1 IIKGFECKPHSQPQWQAALFEK--TRLLCGATLIAPRWLLTAHCL---KPRYIVHLGQHN 55
Db 2 IVGSEANIGSFPMQVSLQYRGHFCGSLISPRWVLTAAHCVGSGDSIRVRLGSHD 61
Qy 56 LQKEEGCEQRTATSPHFGFNNSLPNKDHRNDIMLVKMASPVSTIWAVRPLTL--SSR 113
Db 62 LSSGEE--TQTVKSKVIVHNPYNS-----TYDNDIALLLKLEPEVTLSDTVRPICLPSSGY 116
Qy 114 CVTAGTCLISGWSGTSPPQLRPHLTRCANITIEHOKCENAYPGN--ITDTMVCASVQ 172
Db 117 NVPAGTCTVSGWGTSESSGSLPDTLQEVNPIVSNATCERAYSGGAIIDNMLCAGGLE 176
Qy 173 GKKSCQSDSGGPLVQNS---LOGIISWGODPCAITRKPGVYTKVKYVDWI 222
Db 177 GKKDACQDGGGPLVQNS---LOGIISWGODPCAITRKPGVYTKVKYVDWI 229

RESULT 25
US-10-071-214-49
; Sequence 49, Application US/10071214
; Publication No. US2003006099A1
; GENERAL INFORMATION:
; APPLICANT: HANSSON, Lennart
; APPLICANT: EGELRUD, Torbjorn
; TITLE OF INVENTION: SCCE MODIFIED TRANSGENIC MAMMALS AND THEIR USE AS MODELS OF HUMAN
; FILE REFERENCE: HANSSON-3A
; CURRENT APPLICATION NUMBER: US/10/071,214
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,422
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: DK PA 2001 00218
; PRIOR FILING DATE: 2001-02-09

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; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/242,612
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/242,880
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 60/242,881
; PRIOR FILING DATE: 2000-10-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 97
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Trypsin
; OTHER INFORMATION: Consensus Sequence
US-09-981-151A-97

Query Match          37.4%; Score 470.5; DB 11; Length 217;
Best Local Similarity 44.1%; Pred. No. 3.8e-39;
Matches 100; Conservative 35; Mismatches 77; Indels 15; Gaps 7;

QY 1 IIKGFECKPHSQWQAALFEKTRLLCGATLIAPRWLLTAHCLKPRYIVH--LGQHNLOK 58
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 IVGREAQAGSPFQVQSLQVSSGHFCGGLISENWLTAACHVSGASSVRVVLGEHNLGT 60
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 59 EGGCEQTRATATSFPHGPFNNSLPNKDHNDIMLVKMASPVSIITWAVRPLTI--SSRCVT 116
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 TGTGEQKFDVKLIIVHPNYN-----PTNDIALKLKSPVLGDTVRPICLSASSDLP 114
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 117 AGTSLISGWGSTSPQLRPLHTLRCAITIIHOKCENAYPGNITDTMVCASVQEGGKD 176
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 115 VGTTCVSGWGRTKN--LGTSDTLQEVVVPVSVRETCSRAYSAGGTVDITMTCAGAL-GGKD 171
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 177 SCQDGGGLVCSN-Q-SLOGIISWGQDPCATRKGGYTKVCKYVDWI 222
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 172 ACQDGGGLVCSN-Q-SLOGIISWGQDPCATRKGGYTKVCKYVDWI 217
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 30
US-10-042-865-156
; Sequence 156, Application US/10042865
; Publication No. US20040029216A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Casman, Stacie J
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zhong, Mei
; APPLICANT: Gangolli, Esha A
; APPLICANT: Burgess, Catherine E
; APPLICANT: Patturajan, Meera
; APPLICANT: Vernet, Corine A.M
; APPLICANT: Taylor, Sarah
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Miller, Charles E
; APPLICANT: Guo, Xiaojia
; APPLICANT: Boldog, Ference L
; APPLICANT: Grosse, William M
; APPLICANT: Alsobrook II, John P
; APPLICANT: Gerlach, Valerie L
; APPLICANT: Edinger, Salomit R
; APPLICANT: Rothenberg, Mark E
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John
; APPLICANT: Malvankar, Uriel M
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John
; APPLICANT: Smithson, Glenda
; APPLICANT: Gunther, Erik
```

```
; APPLICANT: Stone, David
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; TITLE OF INVENTION: Using the Same
; FILE REFERENCE: 21402-537
; CURRENT APPLICATION NUMBER: US/10/042,865
; CURRENT FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/260,417
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/260,831
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: 60/272,338
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/274,876
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/284,704
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 264
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 156
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-042-865-156

Query Match          37.4%; Score 470.5; DB 12; Length 217;
Best Local Similarity 44.1%; Pred. No. 3.8e-39;
Matches 100; Conservative 35; Mismatches 77; Indels 15; Gaps 7;

QY 1 IIKGFECKPHSQWQAALFEKTRLLCGATLIAPRWLLTAHCLKPRYIVH--LGQHNLOK 58
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 IVGREAQAGSPFQVQSLQVSSGHFCGGLISENWLTAACHVSGASSVRVVLGEHNLGT 60
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 59 EGGCEQTRATATSFPHGPFNNSLPNKDHNDIMLVKMASPVSIITWAVRPLTI--SSRCVT 116
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 TGTGEQKFDVKLIIVHPNYN-----PTNDIALKLKSPVLGDTVRPICLSASSDLP 114
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 117 AGTSLISGWGSTSPQLRPLHTLRCAITIIHOKCENAYPGNITDTMVCASVQEGGKD 176
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 115 VGTTCVSGWGRTKN--LGTSDTLQEVVVPVSVRETCSRAYSAGGTVDITMTCAGAL-GGKD 171
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 177 SCQDGGGLVCSN-Q-SLOGIISWGQDPCATRKGGYTKVCKYVDWI 222
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 172 ACQDGGGLVCSN-Q-SLOGIISWGQDPCATRKGGYTKVCKYVDWI 217
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 31
US-10-072-012-805
; Sequence 805, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Shinkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Esha
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Colman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol E. A
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grosse, William M.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
```

; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same

; FILE REFERENCE: 21402-258

; CURRENT APPLICATION NUMBER: US/10/072,012

; CURRENT FILING DATE: 2002-01-31

; PRIOR APPLICATION NUMBER: 60/265,102

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: 60/265,514

; PRIOR FILING DATE: 2001-01-31

; PRIOR APPLICATION NUMBER: 60/265,517

; PRIOR FILING DATE: 2001-01-31

; PRIOR APPLICATION NUMBER: 60/265,412

; PRIOR FILING DATE: 2001-01-31

; PRIOR APPLICATION NUMBER: 60/265,395

; PRIOR FILING DATE: 2001-01-31

; PRIOR APPLICATION NUMBER: 60/266,406

; PRIOR FILING DATE: 2001-02-02

; PRIOR APPLICATION NUMBER: 60/266,767

; PRIOR FILING DATE: 2001-02-05

; PRIOR APPLICATION NUMBER: 60/267,057

; PRIOR FILING DATE: 2001-02-07

; PRIOR APPLICATION NUMBER: 60/266,975

; PRIOR FILING DATE: 2001-02-07

; PRIOR APPLICATION NUMBER: 60/267,459

; PRIOR FILING DATE: 2001-02-08

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 1391

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 805

; LENGTH: 217

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Trypsin

; OTHER INFORMATION: Consensus Sequence

US-10-072-012-805

Query Match 37.4%; Score 470.5; DB 12; Length 217;
Best Local Similarity 44.1%; Pred. No. 3.8e-39;
Matches 100; Conservative 35; Mismatches 77; Indels 15; Gaps 7;

Qy 1 IIKFECKPHSQPQWQAALFEKTRLLCGATLIAPRWLLTAHCLKPRYIVH--LGQHNLOK 58

Db 1 IVGREAQAGSFPQVSLQVSSGHFCGSLISENNWLTAAHCVSGASSVRVVLGEHNLGT 60

Qy 59 EBGCEQRTATSPFHGPFNNSLPNKDRNDIMLVKMASPVSIWAVRPLTL--SSRCVT 116

Db 61 TEGTEQKFDVKKIIVHFNYN-----PDTNDIALLLKSPVTLGDTVRPICLPSSASDLP 114

Qy 117 AGTSLISGWGSTSSPOLRPHILRCANITIIHQKCNAYPGNITDTWVCASVQEGGKD 176

Db 115 VGTTCVSGWGRTKN--LGTSDTLQEVVVPVIVSETCRSAYGTVTDTMICAGAL--GGKD 171

Qy 177 SCQDSGGPLVCNQ--SLQGIISWGQDPCATRKPGVTKVKCYVDWI 222

Db 172 ACQDSGGPLVCSGDELGVISWGYG--CAVGNPGVYTRVSRYLDWI 217

RESULT 32

US-10-072-012-813

; Sequence 813, Application US/10072012

; Publication No. US20040033493A1

; GENERAL INFORMATION:

; APPLICANT: Tchernev, Velizar

; APPLICANT: Spytek, Kimberly

; APPLICANT: Zerhusen, Bryan

; APPLICANT: Patturajan, Meera

; APPLICANT: Shimkets, Richard

; APPLICANT: Li, Li

; APPLICANT: Gangolli, Esha

; APPLICANT: Padigaru, Muralidhara

; APPLICANT: Anderson, David W.

; APPLICANT: Rastelli, Luca

; APPLICANT: Miller, Charles E.

; APPLICANT: Gerlach, Valerie

; APPLICANT: Taupier Jr, Raymond J.

; APPLICANT: Gusev, Vladimir Y.

; APPLICANT: Colman, Steven D.

; APPLICANT: Wolenc, Adam R.

; APPLICANT: Pena, Carol E. A.

; APPLICANT: Furtak, Katarzyna

; APPLICANT: Grosse, William M.

; APPLICANT: Alsobrook II, John P.

; APPLICANT: Lepley, Denise M.

; APPLICANT: Rieger, Daniel K.

; APPLICANT: Burgess, Catherine E.

; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same

; FILE REFERENCE: 21402-258

; CURRENT APPLICATION NUMBER: US/10/072,012

; CURRENT FILING DATE: 2002-01-31

; PRIOR APPLICATION NUMBER: 60/265,102

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: 60/265,514

; PRIOR FILING DATE: 2001-01-31

; PRIOR APPLICATION NUMBER: 60/265,517

; PRIOR FILING DATE: 2001-01-31

; PRIOR APPLICATION NUMBER: 60/265,412

; PRIOR FILING DATE: 2001-01-31

; PRIOR APPLICATION NUMBER: 60/265,395

; PRIOR FILING DATE: 2001-01-31

; PRIOR APPLICATION NUMBER: 60/266,406

; PRIOR FILING DATE: 2001-02-02

; PRIOR APPLICATION NUMBER: 60/266,767

; PRIOR FILING DATE: 2001-02-05

; PRIOR APPLICATION NUMBER: 60/267,057

; PRIOR FILING DATE: 2001-02-07

; PRIOR APPLICATION NUMBER: 60/266,975

; PRIOR FILING DATE: 2001-02-07

; PRIOR APPLICATION NUMBER: 60/267,459

; PRIOR FILING DATE: 2001-02-08

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 1391

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 813

; LENGTH: 217

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Trypsin

; OTHER INFORMATION: Consensus Sequence

US-10-072-012-813

Query Match 37.4%; Score 470.5; DB 12; Length 217;

Best Local Similarity 44.1%; Pred. No. 3.8e-39;

Matches 100; Conservative 35; Mismatches 77; Indels 15; Gaps 7;

Qy 1 IIKFECKPHSQPQWQAALFEKTRLLCGATLIAPRWLLTAHCLKPRYIVH--LGQHNLOK 58

Db 1 IVGREAQAGSFPQVSLQVSSGHFCGSLISENNWLTAAHCVSGASSVRVVLGEHNLGT 60

Qy 59 EBGCEQRTATSPFHGPFNNSLPNKDRNDIMLVKMASPVSIWAVRPLTL--SSRCVT 116

Db 61 TEGTEQKFDVKKIIVHFNYN-----PDTNDIALLLKSPVTLGDTVRPICLPSSASDLP 114

Qy 117 AGTSLISGWGSTSSPOLRPHILRCANITIIHQKCNAYPGNITDTWVCASVQEGGKD 176

Db 115 VGTTCVSGWGRTKN--LGTSDTLQEVVVPVIVSETCRSAYGTVTDTMICAGAL--GGKD 171

Qy 177 SCQDSGGPLVCNQ--SLQGIISWGQDPCATRKPGVTKVKCYVDWI 222

Db 172 ACQDSGGPLVCSGDELGVISWGYG--CAVGNPGVYTRVSRYLDWI 217

RESULT 33

US-10-037-417-136

; Sequence 136, Application US/10037417

; Publication No. US20040052806A1

OTHER INFORMATION: Description of Artificial Sequence: Trypsin
US-10-032-189-67

Query Match 37.4%; Score 470.5; DB 14; Length 217;
Best Local Similarity 44.1%; Pred. No. 3.8e-39;
Matches 100; Conservative 35; Mismatches 77; Indels 15; Gaps 7;
QY 1 IIKGECKPHSQWQAALFEKTRLLCGATLIAPRWLLTAHCLKPRYIVH--LGQHNLOK 58
DB 1 IVGREQAQGSFWQVSLQVSSGHFCGSLISENWNVLTAAHCVSGASSVRVLGEHNLGT 60
QY 59 BEGCEQTRTATESPPHGFNNLSFNKDHNDIMLVKMASPVSTWAVRPLTL--SSRCVT 116
DB 61 TEGTEQKFDVKKIIVHFNYN-----PDTNDIALLLKLSPTLGDVTRPICLPSASDLP 114
QY 117 AGTSCLSGWSSTSSPOLRLPHILRCANITIIHOKENAYPGNITDTMVCASVQEGGKD 176
DB 115 VGTTCVSGWGRTKN--LGTSDTLQEVVVPVIVSRCTCRSAYGTVTDTMTCAGAL--GGKD 171
QY 177 SCQDGSGLPLVCNQ-SLQGIISWGQDFCAITRKPVGVTYKVKYDVI 222
DB 172 ACQDGSGLPLVCSDGELGVISWGYG-CAVGNYPGVYTRVSRVLDWI 217

RESULT 35

US-10-074-978A-223
Sequence 223, Application US/10074978A
Publication No. US20040010119A1

GENERAL INFORMATION:

APPLICANT: Leite, Mario
APPLICANT: Spytek, Kimberly A
APPLICANT: Guo, Xiaojia (Sasha)
APPLICANT: Fernandes, Elma
APPLICANT: Li, Li
APPLICANT: Kekuda, Ramesh
APPLICANT: Liu, Xiaohong
APPLICANT: Casman, Stacie
APPLICANT: Boldog, Ferenc
APPLICANT: Patturajan, Meera
APPLICANT: Blalock, Angela
APPLICANT: Ballinger, Robert
APPLICANT: Vernet, Corine
APPLICANT: Tchernev, Velizar T
APPLICANT: Malyankar, Uriel M
APPLICANT: Gusev, Vladimir
APPLICANT: Rastelli, Luca
APPLICANT: Mezes, Peter S
APPLICANT: Ellerman, Karen
APPLICANT: Heyes, Melvin P
APPLICANT: Herrman, John
APPLICANT: Pena, Carol E A
APPLICANT: Shinkets, Richard A
APPLICANT: Taupier Jr, Raymond J
APPLICANT: Moore, No. US20040010119A1lie

APPLICANT: Shenoy, Suresh

APPLICANT: Edinger, Shlomit

APPLICANT: Gunther, Erik

APPLICANT: Stone, Dave

APPLICANT: Millet, Isabelle

APPLICANT: Peyman, John

APPLICANT: Smithson, Glennda

FILE REFERENCE: 21402-269

TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME

CURRENT APPLICATION NUMBER: US/10/074,978A

PRIOR FILING DATE: 2003-01-07

PRIOR APPLICATION NUMBER: 60/268,221

PRIOR FILING DATE: 2001-02-12

PRIOR APPLICATION NUMBER: 60/335,109

PRIOR FILING DATE: 2001-10-31

PRIOR APPLICATION NUMBER: 60/312,284

PRIOR FILING DATE: 2001-08-14

PRIOR APPLICATION NUMBER: 60/268,496

PRIOR FILING DATE: 2001-02-13
PRIOR APPLICATION NUMBER: 60/276,703
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/330,293
PRIOR FILING DATE: 2001-10-18
PRIOR APPLICATION NUMBER: 60/322,127
PRIOR FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: 60/280,899
PRIOR FILING DATE: 2001-04-02
PRIOR APPLICATION NUMBER: 60/310,797
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: 60/268,646
PRIOR FILING DATE: 2001-02-14
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 547
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 223
LENGTH: 217
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Trypsin-like
OTHER INFORMATION: serine protease domain sequence
US-10-074-978A-223

Query Match 37.4%; Score 470.5; DB 15; Length 217;

Best Local Similarity 44.1%; Pred. No. 3.8e-39;

Matches 100; Conservative 35; Mismatches 77; Indels 15; Gaps 7;

QY 1 IIKGECKPHSQWQAALFEKTRLLCGATLIAPRWLLTAHCLKPRYIVH--LGQHNLOK 58
DB 1 IVGREQAQGSFWQVSLQVSSGHFCGSLISENWNVLTAAHCVSGASSVRVLGEHNLGT 60
QY 59 BEGCEQTRTATESPPHGFNNLSFNKDHNDIMLVKMASPVSTWAVRPLTL--SSRCVT 116
DB 61 TEGTEQKFDVKKIIVHFNYN-----PDTNDIALLLKLSPTLGDVTRPICLPSASDLP 114
QY 117 AGTSCLSGWSSTSSPOLRLPHILRCANITIIHOKENAYPGNITDTMVCASVQEGGKD 176
DB 115 VGTTCVSGWGRTKN--LGTSDTLQEVVVPVIVSRCTCRSAYGTVTDTMTCAGAL--GGKD 171
QY 177 SCQDGSGLPLVCNQ-SLQGIISWGQDFCAITRKPVGVTYKVKYDVI 222
DB 172 ACQDGSGLPLVCSDGELGVISWGYG-CAVGNYPGVYTRVSRVLDWI 217

RESULT 36

US-10-055-569A-97

Sequence 97, Application US/10055569A

Publication No. US20040024181A1

GENERAL INFORMATION:

APPLICANT: Gangolli, Esha A

APPLICANT: Spytek, Kimberly A

APPLICANT: Gilbert, Jennifer

APPLICANT: Casman, Stacie

APPLICANT: Blalock, Angela

APPLICANT: Li, Li

APPLICANT: Vernet, Corine

APPLICANT: Shenoy, Suresh

APPLICANT: Mishra, Vishnu S

APPLICANT: Furtak, Katarzyna

APPLICANT: Gerlach, Valerie L

APPLICANT: Edinger, Shlomit

APPLICANT: Malyankar, Uriel

APPLICANT: Stone, David

APPLICANT: Millet, Isabelle

APPLICANT: Smithson, Glennda

APPLICANT: Gunther, Erik

APPLICANT: Ellerman, Karen

APPLICANT: Padigaru, Muralidhara

APPLICANT: Taupier Jr., Raymond J

APPLICANT: Anderson, David W

TITLE OF INVENTION: No. US20040024181A1el Human Proteins, Polynucleotides Encoding The

```
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 21402-191
; CURRENT APPLICATION NUMBER: US/10/055,569A
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 60/243,642
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: 60/243,320
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: 60/243,592
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: 60/243,681
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: 60/243,863
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: 60/244,443
; PRIOR FILING DATE: 2000-10-31
; PRIOR APPLICATION NUMBER: 60/245,029
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 60/244,995
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 60/245,293
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: 60/245,315
; PRIOR FILING DATE: 2000-11-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 97
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-055-569A-97

Query Match          37.4%; Score 470.5; DB 16; Length 217;
Best Local Similarity 44.1%; Pred. No. 3.8e-39;
Matches 100; Conservative 35; Mismatches 77; Indels 15; Gaps 7;

Qy 1 IIKGFCKPHSQPQWQALFEKTRLLCGATLIAPRWLLTAHCLKPRYIVH--LQGHNLQK 58
Db 1 IVGREGAAGFPWQVSLQVSSGHFCGSLISENWLTAACHVSGASSVRVVLGEHNLGT 60
Qy 59 EGCQTRTATESFPHGPNNSLPNKDHRNDIMLVKMASPVISITWAVRPLTL--SSRCVT 116
Db 61 TEGTEQKFDVKIIVHPNYN-----PTNDIALKLKSPVTLGDTVRPICLPSSADLP 114
Qy 117 AGTSLISGWSTSPQLRPLHPTLRCAITIIHOKCENAYPGNITDTMVCASVQEGGKD 176
Db 115 VGTTCVSGWGRTKN--LGTSDTLQEVVVPVSVRETCSAYGCTVYDTMI CAGAL-CK 171
Qy 177 SCQGSGLPLVCNQ-SLOGIISWGDQDPCATRKPGVYTKVKYVDWI 222
Db 172 ACQGSGLPLVCSDGELVGSWGYG-CAVGNYPGVYTRVSRYLWI 217

RESULT 37
US-10-262-511-104
; Publication 104, Application US/10262511
; Publication No. US20040038223A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: Feynman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda

; APPLICANT: Zernusen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Catterton, Elina
; APPLICANT: Ji, Weizhen
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Leach, Martin D.
; APPLICANT: Agee, Michele L.
; APPLICANT: Berghs, Constance
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-462C
; CURRENT APPLICATION NUMBER: US/10/262,511
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/373,815
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/381,642
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/373,260
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,826
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,435
; PRIOR FILING DATE: 2001-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 104
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-511-104

Query Match          37.2%; Score 468; DB 12; Length 224;
Best Local Similarity 42.9%; Pred. No. 7e-39;
Matches 87; Conservative 33; Mismatches 77; Indels 6; Gaps 2;

Qy 1 IIKGFCKPHSQPQWQALFEKTRLLCGATLIAPRWLLTAHCLKPRYIVHLGQHNLQKEE 60
Db 16 IIDGAPCARGSHPWQVALLSGNQLHCGGVLVNERWVLTAAHCKMNEVTVHLGSDTLGDRR 75
Qy 61 GCQTRTATESFPHGPNNSLPNKDHRNDIMLVKMASPVISITWAVRPLTLSSSCVTAGTS 120
Db 76 A--QRIKASKSFRRPGYS---TQTHVNDLMLVKLNSQARLSSMWKVRLPFSCEPFGIT 129
Qy 121 CLISGWSTSPQLRPLHPTLRCAITIIHOKCENAYPGNITDTMVCASVQEGGKDCSQG 180
Db 130 CTVSGWGTITSPDVTTFPSDLMLCVDVKLISPDQCTKYKDKLENSMLCAGIPDSKKNACNG 189
Qy 181 DSGGLPLVCNOSLQGIISWGDQDPC 203
Db 190 DSGGLPLVCRGTQLGLVSWGTFFC 212

RESULT 38
US-10-051-874-102
; Sequence 102, Application US/10051874
; Publication No. US20040005557A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Alsobrook II, John P
; APPLICANT: Colman, Steven D
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Boldog, Ferenc
; APPLICANT: Vernet, Corine AM
; APPLICANT: Li, Li
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Casman, Stacie J
; APPLICANT: Guo, Xiaojia Sasha
; APPLICANT: Edinger, Shlomit R
; APPLICANT: MacDougall, John R
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Patturajan, Meera
; APPLICANT: Shinkets, Richard A
; APPLICANT: Pena, Carol EA
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Millet, Isabelle
; APPLICANT: Miller, Charles E
; APPLICANT: Lepley, Denise M
; APPLICANT: Smithson, Glennda
; APPLICANT: Baumgartner, Jason C
; APPLICANT: Herrman, John L
; APPLICANT: Peyman, John A
; APPLICANT: Gorman, Linda
; APPLICANT: Mezes, Peter D
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Gerlach, Valerie
; APPLICANT: Grosse, William M
; APPLICANT: Liu, Xiaochong
; APPLICANT: Ellertman, Karen
; APPLICANT: Rothenberg, Mark
; APPLICANT: Stone, David J
; APPLICANT: Burgess, Catherine E
; TITLE OF INVENTION: PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS OF
; FILE REFERENCE: 21402-245
; CURRENT APPLICATION NUMBER: US/10/051,874
; PRIOR FILING DATE: 2002-09-25
; PRIOR FILING DATE: 2001-02-14
; PRIOR FILING DATE: 2001-09-27
; PRIOR FILING DATE: 2001-01-18
; PRIOR FILING DATE: 2001-02-28
; PRIOR FILING DATE: 2001-01-18
; PRIOR FILING DATE: 2001-03-16
; PRIOR FILING DATE: 2001-05-17
; PRIOR FILING DATE: 2001-10-18
; PRIOR FILING DATE: 2001-03-31
; PRIOR FILING DATE: 2001-01-16
; NUMBER OF SEQ ID NOS: 269
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 102
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Trypsin domain
; OTHER INFORMATION: sequence
US-10-051-874-102

```

```

Query Match 37.0%; Score 465.5; DB 15; Length 215;
Best Local Similarity 44.2%; Pred. No. 1.2e-38;
Matches 99; Conservative 34; Mismatches 76; Indels 15; Gaps 7;

QY 4 GFECKPHSQWQAALFEKTRLLCGATLIAPRWLLTAACHLCKPRIVH--LGOHNLQKEEG 61
Db 2 GREAAQGSFPQWVSLQVSSGHFCGSLISENWVITAACHVCSSASSVRVLTGEHNLGTTEG 61

QY 62 CEQRTATSEPPHFGFNNSLPNKHNDIMLVKMASPVSTWAVRPLTL--SSRCVVTAGT 119
Db 62 TEQKFDVKKIIVHENY-----PDTNDIALLLKLSPTVLGDTVRPICLPSASDLPVGT 115

QY 120 SCLISGWSSTSPQLRPLPHILRCANIYIIHOKENAYPGNITDTWVCASVQSGGKDCQ 179
Db 116 TCSVSGWGRTKN--LGTSDTLQEVVVPVIVSRRETCRSAYGGTVTDTMICAGAL--GGKDACQ 172

QY 180 GDSGGPLVCNQ--SLQGIISWGQDPCAITRKPVGVTYKVKYVDWI 222
Db 173 GDSGGPLVCSGDELGVISWGYG--CAVGNYPGVYTVRSRYLDWI 215

RESULT 39
US-10-325-745-4
; Sequence 4, Application US/10325745
; Publication No. US20030135028A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: Human Serine Protease and Serpin Polypeptides
; FILE REFERENCE: PF391D1
; CURRENT APPLICATION NUMBER: US/10/325,745
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 09/244,111
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: US 60/073,961
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 207
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-325-745-4

Query Match 36.8%; Score 463; DB 14; Length 207;
Best Local Similarity 44.6%; Pred. No. 2e-38;
Matches 87; Conservative 34; Mismatches 70; Indels 4; Gaps 3;

QY 32 APRW--LLTAACHLKPRIYIVHLCQHNLOKEGCEQTRTATESPHFGFNNSLPNKHND 89
Db 9 AKTMMFLLLGGAWAGKYTVRLGDHSLQNKDGEQEPVQVQSIHPHCYNSS--DVEDHND 67

QY 90 IMLVKMASPVSTWAVRPLTLSSRCVVTAGTSCLSISGWSSTSPQLRPLPHILRCANITIE 149
Db 68 LMLQLRQASLGSVKYKPSLADHCTQLAESAFSQAQGVTVSPRENFPTLNCAEVKSPP 127

QY 150 HKCENAYPGNITDTWVCASVQSGGKDCSQGDSGGPLVNCQSLQGIISWGQDPCAITRKP 209
Db 128 QKKCEDAYPGQITDGMVYAGSSKGA--DTCQDSDGGLVCDGALQGITSWGSDPCGRSDXP 186

QY 210 GVTYKVKYVDWIQE 224
Db 187 GVTNICYRLDWIKK 201

RESULT 40
US-10-004-378A-147
; Sequence 147, Application US/10004378A
; Publication No. US20030228301A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Furtak, Kazaryna
; APPLICANT: Perna, Amanda
; APPLICANT: Patturajan, Meera

```

APPLICANT: Shimkets, Richard A
APPLICANT: Guo, Xiaojia Sasha
APPLICANT: Casman, Stacie J
APPLICANT: Burgess, Catherine E
APPLICANT: Malyankar, Uriel M
APPLICANT: Tchernev, Vellizar T
APPLICANT: Vernet, Corrine A
APPLICANT: Spytek, Kimberly A
APPLICANT: Ages, Michele
APPLICANT: Rastelli, Luca
APPLICANT: Shenoy, Suresh G
APPLICANT: Grosse, William M
APPLICANT: Alsbrook II, John P
APPLICANT: Lepley, Denise M
APPLICANT: Gerlach, Valerie
APPLICANT: Edinger, Schlomit
APPLICANT: MacDougall, John R
APPLICANT: Feyman, John A
APPLICANT: Gunther, Erik
APPLICANT: Stone, David J
APPLICANT: Ellerman, Karen
APPLICANT: Gangolli, Esha A
TITLE OF INVENTION: No. US20030228301A1el Human Proteins, Polynucleotides Encoding TH
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 21402-179
CURRENT APPLICATION NUMBER: US/10/004,378A
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 60/242,882
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: 60/242,765
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: 60/300,206
PRIOR FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: 60/242,789
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: 60/242,768
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: 60/242,767
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: 60/243,622
PRIOR FILING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: 60/273,047
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 60/243,591
PRIOR FILING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: 60/243,950
PRIOR FILING DATE: 2000-10-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 191
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 147
LENGTH: 207
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Trypsin domain
US-10-004-378A-147

Query Match 36.5%; Score 459.5; DB 15; Length 207;
Best Local Similarity 44.7%; Pred. NO. 4.6e-38;
Matches 97; Conservative 33; Mismatches 72; Indels 15; Gaps 7;

QY 11 SOPWQALPEKTELLCGATLIAPRWLLTAHCKLPYIVH--LGOHNLQKEGCEQTRTA 68
Db 1 SPFWQVSLQVSGHFGCGSLIENWVLTAAHCVSGASSVRVVLGHNLTGTEGQKEDV 60
QY 69 TESFPHPGNNSLPNKDHNDIMLVKMASPVISITWAVREPLTL--SSRCVTAQTSCLISGW 126
Db 61 KKIIVHPNPN-----PDNDIALALKSPVTLGDTVRPICLPASSDDLPGVTTCSVSGW 114
QY 127 GSTSSQPLRLPHTLRCAITIEHQKCNAYPGNITDTWVCASVQEGKDCQGGSGGPL 186

Db 115 GRTKN--LGTSDTLQEVVPIVSRETCSRSAYGTVTDMICAGAL-GGKDACQDGGGPL 171
QY 187 VCNQ-SLQGIISWGQDPFCATRKPGYVTKYKYVDWI 222
Db 172 VCSDELGVISWGYG-CAVGNTPGVTVRVSRYLDWI 207

RESULT 41
US-10-036-371-8
Sequence 8, Application US/10036371
Publication NO. US20020141987A1
GENERAL INFORMATION:
APPLICANT: BJARNARSON, JON B.
TITLE OF INVENTION: FISH SERINE PROTEINASES AND THEIR PHARMACEUTICAL AND
TITLE OF INVENTION: COSMETIC USE
FILE REFERENCE: 81691/284960
CURRENT APPLICATION NUMBER: US/10/036,371
CURRENT FILING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: 09/411,688
PRIOR FILING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: 5086/99
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 225
TYPE: PRT
ORGANISM: Gadus sp.
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (9)
OTHER INFORMATION: K or R
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (24)
OTHER INFORMATION: Y or F
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (32)
OTHER INFORMATION: K or E
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (33)
OTHER INFORMATION: D or Q
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (64)
OTHER INFORMATION: Y or F
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (71)
OTHER INFORMATION: I or unknown
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (82)
OTHER INFORMATION: N or D
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (92)
OTHER INFORMATION: K or E
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (123)
OTHER INFORMATION: A or D
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (136)
OTHER INFORMATION: V or C
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (13E)
OTHER INFORMATION: N or S
FEATURE:

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/ NAME/KEY: MOD_RES
/ LOCATION: (204)
/ OTHER INFORMATION: H or N
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (212)
/ OTHER INFORMATION: M, V or C
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (224)
/ OTHER INFORMATION: N or S
US-10-036-371-8

Query Match 35.9%; Score 451; DB 13; Length 225;
Best Local Similarity 41.0%; Pred. No. 3.7e-37;
Matches 94; Conservative 38; Mismatches 87; Indels 10; Gaps 6;

Qy 1 IIKGFCKPHSOPQOALFEKTRLLCGATLIAPRWLLTAHCLKPRYIVHLGQHNLOKEE 60
Db 1 IVGGFECTXSHQHQVSL-NSGVHXCGSLNXXVWSAAHCYKSVLRVLGHEHHRVNE 59

Qy 61 GCEQTRTATESFPHPGFNNLPHKNDHNDIMLVKMASPVSIITWAVRPLTLSSRCVTVAGTS 120
Db 60 GTEQXISSSVXRPNYS---SYNIXNDIMLIKTXPATLNGYVHAVALPTECAADATM 115

Qy 121 CLISGWGSTSPQLRPHTRCANITIEHQKENAY-PGNIITDTWVCASVQBGKDSQ 179
Db 116 CTVSGWNTWS-SVXDGDQLXLPLTLSHADCANSGPGMITQSMFCAGYLEGGKDSQ 174

Qy 180 GDSGGLVNCQSLQ--GIISWGDPCAITRKPGVYTKVKYVDWIOETM 226
Db 175 GDSGPPVGVNGVLQGVGVSWGYG-CAERXPVGYYAKYXVLSGWVDTM 222

RESULT 42
US-09-759-143-176
; Sequence 176, Application US/09759143
; Patent No. US2002002248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 176
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(205)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-759-143-176

Query Match 35.9%; Score 447.5; DB 9; Length 205;
Best Local Similarity 39.9%; Pred. No. 7.4e-37;
Matches 83; Conservative 44; Mismatches 74; Indels 7; Gaps 3;

Qy 21 KTRLLCGATLIAPRWLLTAHCLKPRYIVHLGQHNLO-KEEGCEQTRTATESFPHPGFNN 79
Db 2 ENELFCGVLVHPQWVLSAAHCFQNSYTIIGLHLSLEADQEPGQMVVEASLSVRHPEYNR 61

Qy 80 SLPNKDHRNDIMLVKMASPVSIITWAVRPLTLSSRCVTVAGTSCLISGWGSTSPQLRPH 139
Db 62 LL----LANDMLMLKLDSESVESDTIRISIASOCPAGNSCLVSGHGLLANG--RMPTV 115

Qy 140 LRCANITIEHQKENAYPGNIITDTWVCASVQBGKDSQDSCGGLVNCQSLGIISWG 199
Db 116 LHCNVSVVSVXKSLYDPLYPHSMFCAGGQDQKDCNCGDGPLICNGYLQGLVSGF 175

Qy 200 QDPCAITRKPGVYTKVKYVDWIOETMK 227
Db 176 KAPCQGLGVPGYTNLCKFTWIEKTVQ 203

RESULT 43
US-09-780-669-176
; Sequence 176, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 176
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(205)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-780-669-176

Query Match 35.6%; Score 447.5; DB 9; Length 205;
Best Local Similarity 39.9%; Pred. No. 7.4e-37;
Matches 83; Conservative 44; Mismatches 74; Indels 7; Gaps 3;

Qy 21 KTRLLCGATLIAPRWLLTAHCLKPRYIVHLGQHNLO-KEEGCEQTRTATESFPHPGFNN 79
Db 2 ENELFCGVLVHPQWVLSAAHCFQNSYTIIGLHLSLEADQEPGQMVVEASLSVRHPEYNR 61

Qy 80 SLPNKDHRNDIMLVKMASPVSIITWAVRPLTLSSRCVTVAGTSCLISGWGSTSPQLRPH 139
Db 116 LHCNVSVVSVXKSLYDPLYPHSMFCAGGQDQKDCNCGDGPLICNGYLQGLVSGF 175

Qy 200 QDPCAITRKPGVYTKVKYVDWIOETMK 227
Db 176 KAPCQGLGVPGYTNLCKFTWIEKTVQ 203
```

Db 62 LL-----LANDMLIKLDESVSSEDTIRSIASQCTAGNSCLVSGWGLLANG--RMPTV 115

QY 140 LRCANITIIHOKCENAYPGNITDTMVCASVOEGKDSQCGSGPLVCNOSLOGIISWG 199

Db 116 LHCNVSVVSEKXVCKLYDPLYPHPSMFCAGGQDQKDSGGLICNGYLGQVLSFG 175

QY 200 QDPCAITRKPGVYTKVCKYVDWIQETMK 227

Db 176 KAPCGQLGVPGVYTNLCKFTWIEKTVQ 203

RESULT 44

US-09-030-606-176

Sequence 176, Application US/09030606

Patent No. US20020081580A1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: Dillon, Davin C.

TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS

NUMBER OF SEQUENCES: 224

CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED AND BERRY LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98104

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/030,606

FILING DATE: 25-FEB-1998

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Maki, David J.

REGISTRATION NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 210121.428C3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 176:

SEQUENCE CHARACTERISTICS:

LENGTH: 205 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

US-09-030-606-176

Query Match 35.6%; Score 447.5; DB 9; Length 205;

Best Local Similarity 39.9%; Pred. No. 7.4e-37;

Matches 83; Conservative 44; Mismatches 74; Indels 7; Gaps 3;

21 KTRLGCGATLIAPRWLLTAHCLKPRYIVHLGCHNLQ-KEEGCEQTRTATESFPHGPN 79

2 ENELFCGVLVHPQWLSAAHCFQNSYITGLHLSLEADQEPGSQWVEASLSVRHPEYNR 61

80 SLPNKHNRNDIMLVKASPVSIWAVRPLTLSSRCVTAGTSCILISGWSGTSPPQLRLPHT 139

62 LL-----LANDMLIKLDESVSSEDTIRSIASQCTAGNSCLVSGWGLLANG--RMPTV 115

140 LRCANITIIHOKCENAYPGNITDTMVCASVOEGKDSQCGSGPLVCNOSLOGIISWG 199

116 LHCNVSVVSEKXVCKLYDPLYPHPSMFCAGGQDQKDSGGLICNGYLGQVLSFG 175

200 QDPCAITRKPGVYTKVCKYVDWIQETMK 227

176 KAPCGQLGVPGVYTNLCKFTWIEKTVQ 203

RESULT 45

US-09-822-827-176

Sequence 176, Application US/09822827

Patent No. US20020081680A1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

FILE REFERENCE: 210121.534C1

CURRENT APPLICATION NUMBER: US/09/822,827

CURRENT FILING DATE: 2001-03-28

NUMBER OF SEQ ID NOS: 982

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 176

LENGTH: 205

TYPE: PRT

ORGANISM: Homo sapien

FEATURE:

NAME/KEY: VARIANT

LOCATION: (1)...(205)

OTHER INFORMATION: Xaa = Any Amino Acid

US-09-822-827-176

Query Match 35.6%; Score 447.5; DB 9; Length 205;

Best Local Similarity 39.9%; Pred. No. 7.4e-37;

Matches 83; Conservative 44; Mismatches 74; Indels 7; Gaps 3;

21 KTRLGCGATLIAPRWLLTAHCLKPRYIVHLGCHNLQ-KEEGCEQTRTATESFPHGPN 79

2 ENELFCGVLVHPQWLSAAHCFQNSYITGLHLSLEADQEPGSQWVEASLSVRHPEYNR 61

80 SLPNKHNRNDIMLVKASPVSIWAVRPLTLSSRCVTAGTSCILISGWSGTSPPQLRLPHT 139

62 LL-----LANDMLIKLDESVSSEDTIRSIASQCTAGNSCLVSGWGLLANG--RMPTV 115

140 LRCANITIIHOKCENAYPGNITDTMVCASVOEGKDSQCGSGPLVCNOSLOGIISWG 199

116 LHCNVSVVSEKXVCKLYDPLYPHPSMFCAGGQDQKDSGGLICNGYLGQVLSFG 175

200 QDPCAITRKPGVYTKVCKYVDWIQETMK 227

176 KAPCGQLGVPGVYTNLCKFTWIEKTVQ 203

RESULT 46

US-09-115-453-176

Sequence 176, Application US/09115453B

Patent No. US20020090372A1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: Dillon, Davin C.

TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND

TITLE OF INVENTION: METHODS FOR THEIR USE.

FILE REFERENCE: 210121.427C4

CURRENT APPLICATION NUMBER: US/09/115,453B

CURRENT FILING DATE: 1998-07-14

NUMBER OF SEQ ID NOS: 228

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 176

LENGTH: 205

TYPE: PRT

ORGANISM: Homo sapien

FEATURE:

NAME/KEY: VARIANT

LOCATION: (1)...(205)

OTHER INFORMATION: Xaa = Any Amino Acid

US-09-115-453-176

Query Match 35.6%; Score 447.5; DB 9; Length 205;

Best Local Similarity 39.9%; Pred. No. 7.4e-37;

Matches 83; Conservative 44; Mismatches 74; Indels 7; Gaps 3;

Qy 21 KTRLLGATLIAPRWLLTAARCLKPRYIVHLGQHNLO-KEEGCEQTRTATESPPHGFNN 79
 Db 2 ENELFCGVLVHPQWLSAAHCFQNSYTIIGLHLSLEADQEPGSQMVSEASLSVRHPEYNR 61
 Qy 80 SLPNKDRNDIMLVKMASPVSIWAVRPLTLSSRCVTTAGTSCLSGSGTSSPQLRLPHT 139
 Db 62 LL-----LANDMLIKLDESVSSEDTIRSIASQCPAGNSCLVSGWGLLANG--RMPVTV 115
 Qy 140 LRCANITIIHOKCENAYPGNITDTWVCASVQEGGKDSQCGDSGGPLVCNOSLQGIISWG 199
 Db 116 LHCNVSVSVSEKSLYDPLVHPSMFCAGGGQDKDSCNGDSGGPLICNGVILQGLVSFG 175
 Qy 200 QDPCAITRKPGVYTKVCKYVDWIQETMK 227
 Db 176 KAPCGQLGVPGVYTNLCKFTIEWIEKTVQ 203

RESULT 47

US-09-232-880-176
 ; Sequence 176, Application US/09232880
 ; Publication No. US20020192596A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitcham, Jennifer Lynn
 ; TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF
 ; TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE
 ; FILE REFERENCE: 210121.428C6
 ; CURRENT APPLICATION NUMBER: US/09/232.880
 ; CURRENT FILING DATE: 1999-01-15
 ; NUMBER OF SEQ ID NOS: 338
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 176
 ; LENGTH: 205
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 ; FEATURE:
 ; NAME/KEY: VARIANT
 ; LOCATION: (1)...(205)
 ; OTHER INFORMATION: Xaa = Any Amino Acid
 ; US-09-232-880-176

Query Match 35.6%; Score 447.5; DB 9; Length 205;
 Best Local Similarity 39.9%; Pred. No. 7.4e-37;
 Matches 83; Conservative 44; Mismatches 74; Indels 7; Gaps 3;
 Qy 21 KTRLLGATLIAPRWLLTAARCLKPRYIVHLGQHNLO-KEEGCEQTRTATESPPHGFNN 79
 Db 2 ENELFCGVLVHPQWLSAAHCFQNSYTIIGLHLSLEADQEPGSQMVSEASLSVRHPEYNR 61
 Qy 80 SLPNKDRNDIMLVKMASPVSIWAVRPLTLSSRCVTTAGTSCLSGSGTSSPQLRLPHT 139
 Db 62 LL-----LANDMLIKLDESVSSEDTIRSIASQCPAGNSCLVSGWGLLANG--RMPVTV 115
 Qy 140 LRCANITIIHOKCENAYPGNITDTWVCASVQEGGKDSQCGDSGGPLVCNOSLQGIISWG 199
 Db 116 LHCNVSVSVSEKSLYDPLVHPSMFCAGGGQDKDSCNGDSGGPLICNGVILQGLVSFG 175
 Qy 200 QDPCAITRKPGVYTKVCKYVDWIQETMK 227
 Db 176 KAPCGQLGVPGVYTNLCKFTIEWIEKTVQ 203

RESULT 48

US-09-895-793-176
 ; Sequence 176, Application US/09895793
 ; Publication No. US20020192763A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocker, Susan L.

APPLICANT: Jiang, Yugu
 APPLICANT: Kalos, Michael D.
 APPLICANT: Retter, Marc W.
 APPLICANT: Stolk, John A.
 APPLICANT: Day, Craig H.
 APPLICANT: Vedvick, Thomas S.
 APPLICANT: Carter, Darrick
 APPLICANT: Li, Samuel X.
 APPLICANT: Wang, Aijun
 APPLICANT: Skeiky, Yasir A.W.
 APPLICANT: Hepler, William T.
 APPLICANT: Henderson, Robert A.
 APPLICANT: Hural, John
 APPLICANT: McNeill, Patricia D.
 APPLICANT: Houghton, Raymond L.
 APPLICANT: Vinals de Bassols, Carlota
 APPLICANT: Foy, Teresa
 APPLICANT: Fanger, Gary R.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
 FILE REFERENCE: 210121.534C2
 CURRENT APPLICATION NUMBER: US/09/895.793
 CURRENT FILING DATE: 2001-06-29
 NUMBER OF SEQ ID NOS: 982
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 176
 LENGTH: 205
 TYPE: PRT
 ORGANISM: Homo sapien
 FEATURE:
 NAME/KEY: VARIANT
 LOCATION: (1)...(205)
 OTHER INFORMATION: Xaa = Any Amino Acid
 ; US-09-895-793-176

Query Match 35.6%; Score 447.5; DB 9; Length 205;
 Best Local Similarity 39.9%; Pred. No. 7.4e-37;
 Matches 83; Conservative 44; Mismatches 74; Indels 7; Gaps 3;
 Qy 21 KTRLLGATLIAPRWLLTAARCLKPRYIVHLGQHNLO-KEEGCEQTRTATESPPHGFNN 79
 Db 2 ENELFCGVLVHPQWLSAAHCFQNSYTIIGLHLSLEADQEPGSQMVSEASLSVRHPEYNR 61
 Qy 80 SLPNKDRNDIMLVKMASPVSIWAVRPLTLSSRCVTTAGTSCLSGSGTSSPQLRLPHT 139
 Db 62 LL-----LANDMLIKLDESVSSEDTIRSIASQCPAGNSCLVSGWGLLANG--RMPVTV 115
 Qy 140 LRCANITIIHOKCENAYPGNITDTWVCASVQEGGKDSQCGDSGGPLVCNOSLQGIISWG 199
 Db 116 LHCNVSVSVSEKSLYDPLVHPSMFCAGGGQDKDSCNGDSGGPLICNGVILQGLVSFG 175
 Qy 200 QDPCAITRKPGVYTKVCKYVDWIQETMK 227
 Db 176 KAPCGQLGVPGVYTNLCKFTIEWIEKTVQ 203

RESULT 49
 US-09-895-814-176
 ; Sequence 176, Application US/09895814
 ; Publication No. US20020193296A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Jiang, Yugu
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Retter, Marc W.
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Day, Craig H.
 ; APPLICANT: Vedvick, Thomas S.
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Li, Samuel X.

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; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 176
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(205)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-895-814-176

Query Match          35.6%; Score 447.5; DB 9; Length 205;
Best Local Similarity 39.9%; Pred. No. 7.4e-37;
Matches 83; Conservative 44; Mismatches 74; Indels 7; Gaps 3;

QY 21 KTRLCCGATLIAPRWLLTAACHLKPRYIVHLGHNLO-KEEGCEOTRTATSEFPHPGNN 79
Db 2 ENELFCGVLVHPQWVLSAAHCFQNSYTIIGLHLSLEADQEPGSMVEASLSVRHPEYNR 61
QY 80 SLPNKDRNDIMLVKASPVSTWAVRPLTSSRCVVTAGTSCLSISGWGTSPPQLRLPHT 139
Db 62 LL----LANDMLIKLDESVSSEDTRISISIASQCTAGNSCLVSGWGLLANG--RMPTV 115
QY 140 LRCANITIIHQKCNAYPGNITDTMVCASVQEGKDCQGDGSGPLVNCOSLOGIISWG 199
Db 116 LHCNVSVVSEKVCCKLYDPLVHPSMFCAGGQDQKDCNCGDSGGLICNGYLOGLVSFG 175
QY 200 QDPCAITRKPGVYTKVCKYVDWIQETMK 227
Db 176 KAPCGQLGVPGYVTNLCKFTFETVQ 203
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RESULT 50

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US-10-012-896-176
; Sequence 176, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
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; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darriek
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
```

```

; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Wantanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 176
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 127, 204
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-012-896-176

Query Match          35.6%; Score 447.5; DB 13; Length 205;
Best Local Similarity 39.9%; Pred. No. 7.4e-37;
Matches 83; Conservative 44; Mismatches 74; Indels 7; Gaps 3;

QY 21 KTRLCCGATLIAPRWLLTAACHLKPRYIVHLGHNLO-KEEGCEOTRTATSEFPHPGNN 79
Db 2 ENELFCGVLVHPQWVLSAAHCFQNSYTIIGLHLSLEADQEPGSMVEASLSVRHPEYNR 61
QY 80 SLPNKDRNDIMLVKASPVSTWAVRPLTSSRCVVTAGTSCLSISGWGTSPPQLRLPHT 139
Db 62 LL----LANDMLIKLDESVSSEDTRISISIASQCTAGNSCLVSGWGLLANG--RMPTV 115
QY 140 LRCANITIIHQKCNAYPGNITDTMVCASVQEGKDCQGDGSGPLVNCOSLOGIISWG 199
Db 116 LHCNVSVVSEKVCCKLYDPLVHPSMFCAGGQDQKDCNCGDSGGLICNGYLOGLVSFG 175
QY 200 QDPCAITRKPGVYTKVCKYVDWIQETMK 227
Db 176 KAPCGQLGVPGYVTNLCKFTFETVQ 203
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Search completed: June 25, 2004, 15:20:19
Job time : 52 secs
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 26, 2004, 23:45:26 ; Search time 456 Seconds
(without alignment)
23000.591 Million cell updates/sec

Title: US-09-856-320A-2_COPY_54_282.

Perfect score: 1258

Sequence: 1 IIKGFECKPHSQPMQALFE.....GVYIKVKYVDWIQETMKNN 229

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3017426 seqs, 2290544650 residues

Total number of hits satisfying chosen parameters: 2194776

Minimum DB seq length: 0

Maximum DB seq length: 229

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 500 summaries

Command line parameters:

-MODEL=frame+ p2n.spool -DEV=xlh
-O=/cgn2_1/USPTO.spool/US09856320/runat_25062004_124555_1062/app_query.fasta_1.391
-DB=Published Applications NA -QFMT=fastap -SUFFX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=500 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=50 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEADPSIZE=500 -MINLEN=0
-MAXLEN=229 -USR=US09856320 -CGN 1 1 485 @runat_25062004_124555_1062 -NCPU=6
-ICPU=3 -NO MMAP -LARGEOQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US05_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
17: /cgn2_6/ptodata/1/pubpna/US10D_NEW_PUB.seq.*
18: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	287	22.8	158	15	US-10-029-386-23402
2	206	16.4	153	13	US-10-344-394-24
3	202.5	16.1	205	9	US-09-777-564-697
4	202.5	16.1	205	15	US-10-015-219-697
5	194	15.4	178	13	US-10-262-511-57
6	188	14.9	202	15	US-10-029-386-21469
7	171.5	13.6	181	10	US-09-814-353-15407
8	167	13.3	188	15	US-10-029-386-21559
9	164	13.0	154	13	US-10-344-394-14
10	156	12.4	138	15	US-10-029-386-23583
11	153	12.2	203	15	US-10-029-386-24458
12	149.5	11.9	203	9	US-09-960-352-11298
13	138.5	11.0	147	15	US-10-029-386-19717
14	136	10.8	137	13	US-10-344-394-20
15	136	10.8	163	9	US-09-867-701-3234
16	131.5	10.5	216	9	US-09-885-441-16
17	131.5	10.5	216	13	US-10-424-836-16
18	129.5	10.3	154	15	US-10-029-386-23119
19	128.5	10.2	216	15	US-10-029-386-23582
20	124.5	9.9	180	15	US-10-029-386-23379
21	123	9.8	178	15	US-10-275-091-6
22	123	9.8	178	16	US-10-240-460-3
23	122	9.7	173	15	US-10-029-386-21383
24	122	9.7	196	15	US-10-029-386-26364
25	119	9.5	149	15	US-10-029-386-21960
26	117	9.3	180	15	US-10-094-507-21
27	115	9.1	182	9	US-09-864-761-28604
28	114	9.1	184	15	US-10-060-036-3294
29	114	9.1	195	15	US-10-060-036-3490
30	114	9.1	214	15	US-10-060-036-3865
31	113	9.0	205	15	US-10-060-036-3854
32	112	8.9	181	15	US-10-060-036-3798
33	112	8.9	190	15	US-10-060-036-3798
34	111.5	8.9	123	15	US-10-029-386-23643
35	109	8.7	175	15	US-10-029-386-23238
36	109	8.7	218	15	US-10-060-036-4410
37	108	8.6	175	9	US-09-864-761-27190
38	108	8.6	220	9	US-09-923-779-118
39	108	8.6	220	9	US-09-923-779-119
40	108	8.6	220	9	US-09-923-779-124
41	108	8.6	220	9	US-09-923-779-125
42	108	8.6	220	9	US-09-923-779-126
43	108	8.6	220	9	US-09-923-779-127
44	107.5	8.5	176	15	US-10-029-386-14818
45	107	8.5	118	15	US-10-029-386-26680
46	107	8.5	208	9	US-09-923-779-89
47	105	8.3	156	15	US-10-060-036-3583
48	104.5	8.3	138	9	US-09-888-615-58
49	104	8.3	157	15	US-10-060-036-3369
50	103.5	8.2	189	13	US-10-424-599-75219
51	102.5	8.1	161	15	US-10-029-386-24763
52	101.5	8.1	116	9	US-09-864-761-18438
53	101	8.0	177	13	US-10-150-813-82
54	101	8.0	177	13	US-10-139-854-82
55	101	8.0	177	13	US-10-131-403-82
56	101	8.0	177	16	US-10-150-811-82
57	101	8.0	181	13	US-09-771-357-95
58	101	8.0	181	15	US-10-059-579-95
59	101	8.0	224	15	US-10-100-178-2
60	99.5	7.9	167	15	US-10-029-386-26388
61	98	7.8	211	9	US-09-923-779-16
62	97.5	7.8	177	15	US-10-029-386-27142
63	97	7.7	167	9	US-09-885-441-17
64	97	7.7	167	13	US-10-424-836-17
65	96	7.6	65	10	US-09-908-975-25850
66	96	7.6	109	15	US-10-029-386-23346
67	95	7.6	172	9	US-09-864-761-28651
68	95	7.6	172	9	US-09-864-761-28993
69	94	7.5	134	15	US-10-029-386-23262
70	92	7.3	60	10	US-09-908-975-8568
71	92	7.3	134	13	US-09-826-734-71
72	92	7.3	211	15	US-10-029-386-27166

c 73	91	7.2	90	9	US-09-759-143-120	Sequence 120, App	146	76	6.0	65	10	US-09-908-975-1272	Sequence 1272, App
c 74	91	7.2	90	9	US-09-780-669-120	Sequence 120, App	147	76	6.0	65	10	US-09-908-975-1285	Sequence 1285, App
c 75	91	7.2	90	9	US-09-030-606-120	Sequence 120, App	148	76	6.0	65	10	US-09-908-975-25847	Sequence 25847, A
c 76	91	7.2	90	9	US-09-822-827-120	Sequence 120, App	c 149	76	6.0	227	15	US-10-060-036-3555	Sequence 3555, App
c 77	91	7.2	90	9	US-09-115-453-120	Sequence 120, App	150	75	6.0	69	15	US-10-340-860A-24	Sequence 24, Appl
c 78	91	7.2	90	9	US-09-332-880-120	Sequence 120, App	c 151	75	6.0	80	16	US-10-446-065-6	Sequence 6, Appl
c 79	91	7.2	90	9	US-09-895-793-120	Sequence 120, App	c 152	75	6.0	127	10	US-09-991-936-406	Sequence 406, App
c 80	91	7.2	90	9	US-09-895-814-120	Sequence 120, App	153	75	6.0	151	15	US-10-128-966-43	Sequence 43, Appl
c 81	91	7.2	90	14	US-10-012-896-120	Sequence 120, App	154	74	5.9	61	9	US-09-909-320-282	Sequence 282, App
c 82	91	7.2	90	15	US-10-010-940-120	Sequence 120, App	155	74	5.9	61	9	US-09-909-088B-282	Sequence 282, App
c 83	91	7.2	90	15	US-10-144-678A-120	Sequence 120, App	156	74	5.9	61	9	US-09-905-291A-282	Sequence 282, App
c 84	91	7.2	90	15	US-10-294-025-120	Sequence 120, App	157	74	5.9	61	9	US-09-902-853-282	Sequence 282, App
c 85	90	7.2	147	10	US-09-991-936-414	Sequence 414, App	158	74	5.9	61	9	US-09-907-824-282	Sequence 282, App
c 86	89	7.1	102	15	US-10-029-386-23378	Sequence 23378, A	159	74	5.9	61	9	US-09-907-841-282	Sequence 282, App
c 87	86.5	6.9	192	13	US-10-621-901-1300	Sequence 1300, App	160	74	5.9	61	10	US-09-904-011-282	Sequence 282, App
c 88	86	6.8	100	15	US-10-272-665-106	Sequence 106, App	161	74	5.9	61	10	US-09-906-742-282	Sequence 282, App
c 89	86	6.8	100	15	US-10-273-321-106	Sequence 106, App	162	74	5.9	61	10	US-09-906-838-282	Sequence 282, App
c 90	86	6.8	100	15	US-10-272-756-106	Sequence 106, App	163	74	5.9	61	10	US-09-907-613-282	Sequence 282, App
c 91	86	6.8	100	16	US-10-273-228-106	Sequence 106, App	164	74	5.9	61	10	US-09-907-942-282	Sequence 282, App
c 92	86	6.8	120	13	US-10-150-813-100	Sequence 100, App	165	74	5.9	61	10	US-09-904-859-282	Sequence 282, App
c 93	86	6.8	120	13	US-10-139-854-100	Sequence 100, App	166	74	5.9	61	10	US-09-909-204-282	Sequence 282, App
c 94	86	6.8	120	15	US-10-131-409-100	Sequence 100, App	167	74	5.9	61	10	US-09-904-820-282	Sequence 282, App
c 95	86	6.8	120	16	US-10-150-811-100	Sequence 100, App	168	74	5.9	61	10	US-09-904-786-282	Sequence 282, App
c 96	86	6.8	135	9	US-09-888-615-57	Sequence 57, Appl	169	74	5.9	61	10	US-09-906-646-282	Sequence 282, App
c 97	85	6.8	60	15	US-10-281-043-4	Sequence 4, Appl	170	74	5.9	61	10	US-09-903-786-282	Sequence 282, App
c 98	85	6.8	100	15	US-10-272-665-107	Sequence 107, App	171	74	5.9	61	10	US-09-903-786-282	Sequence 282, App
c 99	85	6.8	100	15	US-10-273-321-107	Sequence 107, App	172	74	5.9	61	10	US-09-902-903-282	Sequence 282, App
c 100	85	6.8	100	15	US-10-272-756-107	Sequence 107, App	173	74	5.9	61	10	US-09-903-749A-282	Sequence 282, App
c 101	85	6.8	100	16	US-10-273-228-107	Sequence 107, App	174	74	5.9	61	10	US-09-904-119-282	Sequence 282, App
c 102	85	6.8	120	13	US-10-150-813-99	Sequence 99, Appl	175	74	5.9	61	10	US-09-904-956-282	Sequence 282, App
c 103	85	6.8	120	13	US-10-139-854-99	Sequence 99, Appl	176	74	5.9	61	10	US-09-902-736-282	Sequence 282, App
c 104	85	6.8	120	15	US-10-131-409-99	Sequence 99, Appl	177	74	5.9	61	10	US-09-907-794-282	Sequence 282, App
c 105	85	6.8	120	16	US-10-150-811-99	Sequence 99, Appl	178	74	5.9	61	10	US-09-903-943-282	Sequence 282, App
c 106	84.5	6.7	159	15	US-10-029-386-21076	Sequence 21076, A	179	74	5.9	61	10	US-09-904-462-282	Sequence 282, App
c 107	84	6.7	113	13	US-10-150-813-88	Sequence 88, Appl	180	74	5.9	61	10	US-09-907-925-282	Sequence 282, App
c 108	84	6.7	113	13	US-10-139-854-88	Sequence 88, Appl	181	74	5.9	61	10	US-09-902-692-282	Sequence 282, App
c 109	84	6.7	113	15	US-10-131-409-88	Sequence 88, Appl	182	74	5.9	61	10	US-09-903-520-282	Sequence 282, App
c 110	84	6.7	113	16	US-10-150-811-88	Sequence 88, Appl	183	74	5.9	61	10	US-09-905-056-282	Sequence 282, App
c 111	84	6.7	163	10	US-09-814-353-4906	Sequence 4906, App	184	74	5.9	61	10	US-09-909-064-282	Sequence 282, App
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392	59	4.7	43	15	US-10-013-912A-178	Sequence 178, App	465	56	4.5	209	16	US-10-242-535A-22929	Sequence 22929, A
393	59	4.7	43	15	US-10-015-653A-178	Sequence 178, App	466	55, 5	4.4	159	9	US-09-864-761-17729	Sequence 17729, A
394	59	4.7	43	15	US-10-012-101B-178	Sequence 178, App	467	55, 5	4.4	159	9	US-09-864-761-32766	Sequence 32766, A
395	59	4.7	43	15	US-10-015-480A-178	Sequence 178, App	468	55, 5	4.4	171	13	US-10-085-783A-2552	Sequence 2552, Ap
396	59	4.7	43	15	US-10-015-715A-178	Sequence 178, App	469	55, 5	4.4	171	16	US-10-242-535A-2552	Sequence 2552, Ap
397	59	4.7	43	15	US-10-012-237A-178	Sequence 178, App	470	55, 5	4.4	199	9	US-09-864-761-24850	Sequence 24850, A
398	59	4.7	43	15	US-10-013-908A-178	Sequence 178, App	471	55, 5	4.4	207	9	US-09-960-352-13216	Sequence 13216, A
399	59	4.7	43	15	US-10-015-388A-178	Sequence 178, App	472	55, 5	4.4	207	9	US-09-936-634-26	Sequence 26, Appl
400	59	4.7	43	15	US-10-012-753A-178	Sequence 178, App	473	55, 5	4.4	207	10	US-09-997-182-26	Sequence 26, Appl
401	59	4.7	43	15	US-10-017-385A-178	Sequence 178, App	474	55, 5	4.4	221	9	US-09-997-181-26	Sequence 26, Appl
402	59	4.7	43	15	US-10-007-236A-178	Sequence 178, App	475	55, 5	4.4	221	9	US-09-294-093B-4253	Sequence 4253, Ap
403	59	4.7	43	15	US-10-015-389A-178	Sequence 178, App	476	55, 5	4.4	222	9	US-09-974-300-6493	Sequence 6493, Ap
404	59	4.7	43	16	US-10-015-519A-178	Sequence 178, App	477	55, 5	4.4	229	13	US-10-085-783A-11784	Sequence 11784, A
405	59	4.7	43	16	US-10-015-915A-178	Sequence 178, App	478	55, 5	4.4	229	16	US-10-242-535A-11784	Sequence 11784, A
406	59	4.7	43	16	US-10-015-394A-178	Sequence 178, App	479	55	4.4	51	9	US-09-759-143-793	Sequence 733, App
407	59	4.7	43	16	US-10-015-390A-178	Sequence 178, App	480	55	4.4	51	9	US-09-780-669-793	Sequence 733, App
408	59	4.7	43	16	US-10-006-746A-178	Sequence 178, App	481	55	4.4	51	9	US-09-822-827-793	Sequence 733, App
409	59	4.7	43	16	US-10-011-795A-178	Sequence 178, App	482	55	4.4	51	9	US-09-835-793-793	Sequence 733, App
410	59	4.7	43	16	US-10-012-231A-178	Sequence 178, App	483	55	4.4	51	9	US-09-895-814-793	Sequence 733, App
411	59	4.7	60	15	US-10-281-043-3	Sequence 3, Appl	484	55	4.4	51	14	US-10-012-896-793	Sequence 733, App
412	59	4.7	65	10	US-09-908-975-25900	Sequence 25900, A	485	55	4.4	51	15	US-10-144-678A-793	Sequence 733, App
413	59	4.7	192	9	US-09-815-343-681	Sequence 681, App	486	55	4.4	51	15	US-10-294-025-793	Sequence 733, App
414	59	4.7	192	9	US-09-815-343-1031	Sequence 1031, App	487	55	4.4	129	13	US-10-085-783A-21017	Sequence 21017, A
415	59	4.7	192	9	US-09-920-300A-944	Sequence 944, App	488	55	4.4	129	16	US-10-242-535A-21017	Sequence 21017, A
416	59	4.7	192	13	US-10-097-105-681	Sequence 681, App	489	55	4.4	150	10	US-09-535-459-1270	Sequence 1270, Ap
417	59	4.7	192	13	US-10-097-105-1031	Sequence 1031, App	490	55	4.4	192	9	US-09-920-300A-739	Sequence 739, App
418	59	4.7	192	14	US-10-033-528-944	Sequence 944, App	491	55	4.4	192	14	US-10-033-528-739	Sequence 739, App
419	59	4.7	192	15	US-10-099-926-944	Sequence 944, App	492	55	4.4	192	15	US-10-099-926-739	Sequence 739, App
420	59	4.7	193	13	US-10-424-599-26008	Sequence 26008, A	493	55	4.4	195	9	US-09-960-352-5905	Sequence 5905, Ap
421	59	4.7	196	9	US-09-815-343-935	Sequence 935, App	494	55	4.4	213	13	US-10-424-599-32484	Sequence 32484, A
422	59	4.7	196	13	US-10-097-105-935	Sequence 935, App	495	55	4.4	222	9	US-09-864-761-32393	Sequence 32393, A
423	59	4.7	217	15	US-10-029-386-26216	Sequence 26216, A	496	55	4.4	222	9	US-09-864-761-32393	Sequence 32393, A
424	58, 5	4.7	202	13	US-10-424-599-113525	Sequence 113525	497	55	4.4	225	11	US-09-864-761-32393	Sequence 2551, Ap
425	58, 5	4.7	208	13	US-10-085-783A-1085	Sequence 1085, App	498	55	4.4	225	11	US-09-864-761-32393	Sequence 2551, Ap
426	58, 5	4.7	208	16	US-10-242-535A-1085	Sequence 1085, App	499	54, 5	4.3	193	13	US-10-424-599-72239	Sequence 72239, A
427	58, 5	4.7	218	13	US-10-027-632-279224	Sequence 279224,	500	54, 5	4.3	212	15	US-10-299-497-10	Sequence 10, Appl
428	58, 5	4.7	218	16	US-10-027-632-279224	Sequence 279224,				218	15	US-10-029-386-23914	Sequence 23914, A
429	57, 5	4.6	147	13	US-10-424-599-16336	Sequence 16336, A							
430	57, 5	4.6	184	15	US-10-029-386-24444	Sequence 24444, A							
431	57, 5	4.6	195	13	US-10-085-783A-3679	Sequence 3679, App							
432	57, 5	4.6	195	16	US-10-242-535A-3679	Sequence 3679, App							
433	57, 5	4.6	198	13	US-10-424-599-57894	Sequence 57894, A							
434	57	4.5	60	10	US-09-908-975-8758	Sequence 8758, App							
435	57	4.5	65	10	US-09-908-975-1284	Sequence 1284, App							
436	57	4.5	125	13	US-10-150-813-94	Sequence 94, Appl							
437	57	4.5	125	13	US-10-139-854-94	Sequence 94, Appl							

RESULT 1

US-10-029-386-23402
; Sequence 23402, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn., Sharron G.

ALIGNMENTS


```
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEWICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 23402
; LENGTH: 158
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR19.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.88
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.9
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
; OTHER INFORMATION: SWISSPROT HIT: Q9UBX7, EVALUE 8.00e-27
; OTHER INFORMATION: EST HUMAN HIT: AA436049.1, EVALUE 6.00e-82
; OTHER INFORMATION: NT HIT: g114755026, EVALUE 6.00e-84
US-10-029-386-23402

Alignment Scores:
Pred. No.: 8,73e-26 Length: 158
Score: 287.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 22.81% Indels: 0
DB: 15 Gaps: 0

US-09-856-320A-2_COPY_54_282 (1-229) x US-10-029-386-23402 (1-158)
QY 179 GlnGlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrp 198
Db 2 CAGGGTGACTCCGGGGGCCCTCTGGTCTGTACCAAGTCTCTCAAGGCATTATCTCTGG 61
QY 199 GlnGlyAspProCysAlaIleThrArgLysProGlyValThyThrLysValCysLysTyr 218
Db 62 GGCAGGATCCGTGTGCGATCACCCGAAAGCTGGTGTACACGAAAGTCTGCAATAT 121
QY 219 ValAspTrpIleGlnGluThrMetLysAsnAsn 229
Db 122 GTGGACTGTCCAGGAGCAGATGAAGAACAT 154

RESULT 2
US-10-344-394-24
; Sequence 24, Application US/10344394
; Publication No. US20040058342A1
; GENERAL INFORMATION:
; APPLICANT: Yousef, George M.
; APPLICANT: Diamandis, Eleftherios P.
; TITLE OF INVENTION: NOVEL KALLIKREIN GENE
; FILE REFERENCE: 11757.51USWO
; CURRENT APPLICATION NUMBER: US/10/344,394
; CURRENT FILING DATE: 2003-02-11
; PRIOR FILING DATE: 2001-08-10
; PRIOR FILING DATE: 2000-08-11
; PRIOR FILING DATE: 2000-08-11
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 153
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-344-394-24

Alignment Scores:
Pred. No.: 5,33e-16 Length: 153
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Score: 206.00 Matches: 36
Percent Similarity: 80.00% Conservative: 4
Best Local Similarity: 72.00% Mismatches: 10
Query Match: 16.38% Indels: 0
DB: 13 Gaps: 0

US-09-856-320A-2_COPY_54_282 (1-229) x US-10-344-394-24 (1-153)
QY 180 GlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGly 199
Db 1 GGTGACTCTGGGGAGCCCTGTCTGTGGGGGCATCTCGAGGGCATTGTGCTCTGGGGT 60
QY 200 GlnAspProCysAlaIleThrArgLysProGlyValThyThrLysValCysLysTyrVal 219
Db 61 GAGTCCCTTGTGACACACACCACCAAGCCCTGGTGTATATACCAAGTCTGCCACTTGT 120
QY 220 AspTrpIleGlnGluThrMetLysAsnAsn 229
Db 121 GAGTGGATCAGGGAACCATGAAGAGAAC 130

RESULT 3
US-09-777-564-697
; Sequence 697, Application US/09777564
; Patent No. US20020022591A1
; GENERAL INFORMATION:
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 21021.493
; CURRENT APPLICATION NUMBER: US/09/777,564
; CURRENT FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 1730
; SOFTWARE: FastSeq for Window Version 4.0
; SEQ ID NO 697
; LENGTH: 205
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-777-564-697

Alignment Scores:
Pred. No.: 2,12e-15 Length: 205
Score: 202.50 Matches: 34
Percent Similarity: 73.53% Conservative: 16
Best Local Similarity: 50.00% Mismatches: 17
Query Match: 16.10% Indels: 1
DB: 9 Gaps: 1

US-09-856-320A-2_COPY_54_282 (1-229) x US-09-777-564-697 (1-205)
QY 142 CysAlaAsnIleThrIleIleGluHisGlnLysCysGluAsnAlaTyrProGlyAsnIle 161
Db 4 TGCTCCAGCATCACTATCTCTGAGCCCTAAAGAGTGTGAGGTCTTCTACCTCGCGTGTG 63
QY 162 ThrAspThrMetValCysAlaSerValGlnGluGlyLysAspSerCysGlnGlyAsp 181
Db 64 ACCAACACATGATGTGCTGGACTG---GACCGGGCCAGGACCTTGCACAGTGAC 120
QY 182 SerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGlnAsp 201
Db 121 TCTGAGGCCCCCTGGCCTGTGACGAGACCCCTCCAGGACATCTCTCTGGGGGTGTTAC 180
QY 202 ProCysAlaIleThrArgLysPro 209
Db 181 CCCTGTGGCTCTGCCAGCATCCA 204

RESULT 4
US-10-015-219-697
; Sequence 697, Application US/10015219
; Publication No. US20030008299A1
; GENERAL INFORMATION:
; APPLICANT: Algate, Paul A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
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Alignment Scores:

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; OTHER INFORMATION: EST_HUMAN HIT: BG762809.1, EVALUE 3.00e-77
US-10-029-386-19717

Alignment Scores:
Pred. No.: 7.46e-08 Length: 147
Score: 138.50 Matches: 27
Percent Similarity: 66.67% Conservative: 5
Best Local Similarity: 56.25% Mismatches: 11
Query Match: 11.01% Indels: 5
DB: 15 Gaps: 2

US-09-856-320A-2_COPY_54_282 (1-229) x US-10-029-386-19717 (1-147)

Qy 180 GlyAspSerGlyClyProLeuValCysAsnGlnSer-----LeuGlnGlyIle 195
Db 1 GGTGATTCTGGGGGACCTCTGACCTGCTGCAGCTCGGAGCTGGGTCTCTGGTGGCGG 60
Qy 196 IleSerTrpGlyGlnAspProCysAlaIleThrArgLysProGlyValThrLysVal 215
Db 61 GTGAGCTGGGGCAAGGT---TGTGCTCTGCCCAACCGTCCAGGGTCTACACCACTGTG 117
Qy 216 CysLysTyrValAspTrpIleGln 223
Db 118 GCCACATATAGCCCTGGATTTCAG 141

RESULT 14
US-10-344-394-20
; Sequence 20, Application US/10344394
; Publication No. US20040058342A1
; GENERAL INFORMATION:
; APPLICANT: Yousef, George M.
; TITLE OF INVENTION: NOVEL KALLIKREIN GENE
; FILE REFERENCE: 11757.51USWO
; CURRENT APPLICATION NUMBER: US/10/344,394
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: PCT/CA01/01141
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/224,853
; PRIOR FILING DATE: 2000-08-11
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 20
; LENGTH: 137
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-344-394-20

Alignment Scores:
Pred. No.: 1.36e-07 Length: 137
Score: 136.00 Matches: 23
Percent Similarity: 70.45% Conservative: 8
Best Local Similarity: 52.27% Mismatches: 13
Query Match: 10.81% Indels: 0
DB: 13 Gaps: 0

US-09-856-320A-2_COPY_54_282 (1-229) x US-10-344-394-20 (1-137)

Qy 136 LeuProHisThrLeuArgCysAlaAsnIleThrIleIleGluHisGlnLysCysGluAsn 155
Db 6 CTCCAGATACCTTGCTGCTGCAACATCAGCATTTATCTCGGACACATCTTGTGACAAG 65
Qy 156 AlaTyrProGlyAsnIleThrAspThrMetValCysAlaSerValGlnGluGlyLys 175
Db 66 AGCTACCCAGGGCGCTGACAAACACCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 125
Qy 176 AspSerCysGln 179
Db 126 GAATCTGTGTGAG 137

RESULT 15
US-09-867-701-3234/c
; Sequence 3234, Application US/09867701
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; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3234
; LENGTH: 163
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-867-701-3234

Alignment Scores:
Pred. No.: 1.73e-07 Length: 163
Score: 136.00 Matches: 25
Percent Similarity: 64.81% Conservative: 10
Best Local Similarity: 46.30% Mismatches: 19
Query Match: 10.81% Indels: 0
DB: 9 Gaps: 0

US-09-856-320A-2_COPY_54_282 (1-229) x US-09-867-701-3234 (1-163)
QY 176 AspSerCysGlnGlyAspSerGlyProLeuValCysAsnGlnSerLeuGlnGlyIle 195
Db 163 AACTCTCCAGGGAATTCGGGGCTTGGTCTTCAATGGCTCCGCAAGGGAACCC 104
QY 196 IleSerTrpGlnAspProCysAlaIleThrArgLysProGlyValThrLysVal 215
Db 103 GTGCTCTGGGATATTACCTTGTGCGCGCCCAACAGACCGGTTTCTACAGAACCTC 44
QY 216 CysLysTyrValAspTrpIleGlnGluThrMetLysAsnAsn 229
Db 43 TGCAAGTTCACCAAGTGGATCCAGGAACCATCCAGGCCAAC 2

RESULT 16
US-09-885-441-16
; Sequence 16, Application US/09885441
; Patent No. US20020146407A1
; GENERAL INFORMATION:
; APPLICANT: Xiao, Yonghong
; TITLE OF INVENTION: Regulation of Human Eosinophil Serine
; TITLE OF INVENTION: Protease-1-Like Enzyme
; FILE REFERENCE: 04974.00512
; CURRENT APPLICATION NUMBER: US/09/885,441
; CURRENT FILING DATE: 2001-06-21
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: US 60/212,844
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: US 60/244,171
; PRIOR FILING DATE: 2000-10-31
; PRIOR APPLICATION NUMBER: US 60/279,766
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: PCT/
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 216
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-424-836-16

Alignment Scores:
Pred. No.: 8.98e-07 Length: 216
Score: 131.50 Matches: 25
Percent Similarity: 61.11% Conservative: 8
Best Local Similarity: 46.30% Mismatches: 16
Query Match: 10.45% Indels: 5
DB: 13 Gaps: 2

US-09-856-320A-2_COPY_54_282 (1-229) x US-10-424-836-16 (1-216)
QY 180 GlyAspSerGlyGlyProLeuValCysAsnGlnSer-----LeuGlnGlyIle 195
Db 1 GGTGACTCAGGTGGACCCCTTGGTCTGTGACAGGATCGGACTGTGGTATCAGGTTGGAATC 60
QY 196 IleSerTrpGlnAspProCysAlaIleThrArgLysProGlyValThrLysVal 215
Db 61 GTGAGCTGGGGAATGGAC---TGCGGTCAACCAATCGGCTGTGTGTCTACACCAACATC 117
QY 216 CysLysTyrValAspTrpIleGlnGluThrMetLysAsnAsn 229
Db 118 AGTGTGTACTTCCACTGGATCCGGAGGGTGTATGCCACAGT 159

RESULT 17
US-10-424-836-16
; Sequence 16, Application US/10424836
; Publication No. US20030224430A1
; GENERAL INFORMATION:
; APPLICANT: Xiao, Yonghong
; TITLE OF INVENTION: Regulation of Human Eosinophil Serine
; TITLE OF INVENTION: Protease-1-Like Enzyme
; FILE REFERENCE: 04974.00512
; CURRENT APPLICATION NUMBER: US/10/424,836
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: US/09/885,441
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/212,844
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: US 60/244,171
; PRIOR FILING DATE: 2000-10-31
; PRIOR APPLICATION NUMBER: US 60/279,766
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: PCT/
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 216
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-424-836-16

Alignment Scores:
Pred. No.: 8.98e-07 Length: 216
Score: 131.50 Matches: 25
Percent Similarity: 61.11% Conservative: 8
Best Local Similarity: 46.30% Mismatches: 16
Query Match: 10.45% Indels: 5
DB: 13 Gaps: 2

US-09-856-320A-2_COPY_54_282 (1-229) x US-10-424-836-16 (1-216)
QY 180 GlyAspSerGlyGlyProLeuValCysAsnGlnSer-----LeuGlnGlyIle 195
Db 1 GGTGACTCAGGTGGACCCCTTGGTCTGTGACAGGATCGGACTGTGGTATCAGGTTGGAATC 60
QY 196 IleSerTrpGlnAspProCysAlaIleThrArgLysProGlyValThrLysVal 215
Db 61 GTGAGCTGGGGAATGGAC---TGCGGTCAACCAATCGGCTGTGTGTCTACACCAACATC 117
QY 216 CysLysTyrValAspTrpIleGlnGluThrMetLysAsnAsn 229
Db 118 AGTGTGTACTTCCACTGGATCCGGAGGGTGTATGCCACAGT 159

RESULT 18
US-10-029-386-23119/c
; Sequence 23119, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.

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; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.9
; OTHER INFORMATION: SWISSPROT HIT: P10323, EVALUE 2.00e-29
; OTHER INFORMATION: EST_HUMAN_HIT: B1831427.1, EVALUE 1.00e-114
; OTHER INFORMATION: NT_HIT: M77381.1, EVALUE 1.00e-103
US-10-029-386-233582

Alignment Scores:
Pred. No.: 2,07e-06 Length: 216
Score: 128.50 Matches: 26
Percent Similarity: 59.32% Conservative: 9
Best Local Similarity: 44.07% Mismatches: 17
Query Match: 10.21% Indels: 7
DB: 15 Gaps: 2

US-09-856-320A-2_COPY_54_282 (1-229) x US-10-029-386-233582 (1-216)
QY 177 SerCysGlnGlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGln----- 193
Db 36 TCTGGACAGGAGACAGCGCGGCCCTCTCATGTGCCAAGACAGCAAGAAAGCGCCTAT 95
QY 194 -----GlyIleIleSerTrpGlyGlnAspProCysAlaIleThrArgLysProGly 210
Db 96 GTGGTCGTGGGATCACAGCTGGGGGTAGGC---TGTGCCCGTCCCAAGCGCCCGGA 152
QY 211 ValTyThrIysValCysLysTyrValasPrIleGlnGluThrMetLysAsnAsn 229
Db 153 ATCTACAGCCACCTCGCCCTATCTCACTGATGTCGCTCCAGATTGGTTCTTAAAC 209

RESULT 20
US-10-029-386-23379
; Sequence 23379, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David K.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GI
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 23379
; LENGTH: 180
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR1.3
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.5
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.6
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.7
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.4
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.7
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.2
; OTHER INFORMATION: SWISSPROT HIT: P50342, EVALUE 1.00e-19
; OTHER INFORMATION: EST_HUMAN_HIT: BG953129.1, EVALUE 5.00e-92
; OTHER INFORMATION: NT_HIT: AF233563.3, EVALUE 5.00e-97
US-10-029-386-23379

Alignment Scores:
Pred. No.: 4.9e-06 Length: 180
Score: 124.50 Matches: 25
Percent Similarity: 65.31% Conservative: 7
Best Local Similarity: 51.02% Mismatches: 12
Query Match: 9.90% Indels: 5
DB: 15 Gaps: 2

US-09-856-320A-2_COPY_54_282 (1-229) x US-10-029-386-23379 (1-180)
QY 179 GlnGlyAspSerGlyGlyProLeuValCysAsnGlnSer-----LeuGlnGly 194
Db 9 CAGGACGACTCGGGGGGCCCTCTGTCTCCAGGTGAACGGTGCCTGGGTGCAGGTGGC 68

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CURRENT APPLICATION NUMBER: US/10/240,460
 CURRENT FILING DATE: 2003-04-08
 PRIOR APPLICATION NUMBER: PCT/JP01/02771
 PRIOR FILING DATE: 2001-03-30
 PRIOR APPLICATION NUMBER: JP 2000-111939
 PRIOR FILING DATE: 2000-04-07

Qy 20 ---GluLysThrArgLeuLeuCysGlyAlaThrLeuLeuAlaProArgTrpLeuLeuThr 38
Db 94 GTGCCAGGCGCCCTTCCCTGCTGGAGGCGCCCTGCTTTCAGGCCAGTGGTCACTACT 153
Qy 39 AlaAlaHisCys 42
Db 154 GCTGCTCACTGC 165

RESULT 24
US-10-029-386-26364
; Sequence 26364, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: AEOmica-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 26364
; LENGTH: 196
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR19.3
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5
; OTHER INFORMATION: NT HIT: g114786995, EVALUE 1.00e-106
; OTHER INFORMATION: EST HUMAN HIT: BG656040.1, EVALUE 1.00e-106
; OTHER INFORMATION: SWISSPROT HIT: P06870, EVALUE 8.00e-33
US-10-029-386-26364

Alignment Scores:
Pred. No.: 1,11e-05 Length: 196
Score: 122.00 Matches: 26
Percent Similarity: 62.50% Conservative: 14
Best Local Similarity: 40.62% Mismatches: 16
Query Match: 9.70% Indels: 8
DB: 15 Gaps: 2

US-09-856-320A-2_COPY_54_282 (1-229) x US-10-029-386-26364 (1-196)
Qy 73 ProHisProGlyPheAsnSerLeu-----Proklnslyasp 85
Db 3 CCACACCTGGCTTCAACATGAGCCTCTCGAGAACACACCCGCCAAGCAGACAGGAC 62
Qy 86 HisArgAsnAspIleMetLeuVallyMetAlaSerProVal---SerIleThrTrpAla 104
Db 63 TACAGCCACGACCTCATGCTGCTCGCCTGACAGAGCCTGCTGATACCATCACATGCT 122
Qy 105 ValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuLeuSer 124
Db 123 GTGAAGTGTGAGTGTGCTGAGTGTGCCAGGAAACCCGAGGAGCAGCCTGTGCTTCC 182
Qy 125 GlyTrpGlySer 128
Db 183 GGCTGGGGCAGC 194

RESULT 25
US-10-029-386-21960
; Sequence 21960, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: AEOmica-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 26364
; LENGTH: 196
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR19.3
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5
; OTHER INFORMATION: NT HIT: g114786995, EVALUE 1.00e-106
; OTHER INFORMATION: EST HUMAN HIT: BG656040.1, EVALUE 1.00e-106
; OTHER INFORMATION: SWISSPROT HIT: P06870, EVALUE 8.00e-33
US-10-029-386-26364

FILE REFERENCE: AEOmica-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 21960
LENGTH: 149
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO CHR19.3
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.3
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.8
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.4
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.6
OTHER INFORMATION: EST HUMAN HIT: W58737.1, EVALUE 2.00e-78
OTHER INFORMATION: NT HIT: g115301293, EVALUE 1.00e-78
OTHER INFORMATION: SWISSPROT HIT: P49862, EVALUE 4.00e-25
US-10-029-386-21960

Alignment Scores:
Pred. No.: 1,74e-05 Length: 149
Score: 119.00 Matches: 22
Percent Similarity: 59.52% Conservative: 3
Best Local Similarity: 52.38% Mismatches: 17
Query Match: 9.46% Indels: 0
DB: 15 Gaps: 0

US-09-856-320A-2_COPY_54_282 (1-229) x US-10-029-386-21960 (1-149)
Qy 1 IleIleLysGlyPheGluCysLysProHisSerGlnProTrpGlnAlaLeuPheGlu 20
Db 16 ATTATTGATGGCCGCCCTATGTCAGAGGCTCCACCCATGGCAGGTGGCCCTGCTCAGT 75
Qy 21 LysThrArgLeuLeuCysGlyAlaThrLeuLeuAlaProArgTrpLeuLeuThrAla 40
Db 76 GGCAATCAGCTCCACTGGGAGGCGCTCTGTCAATGAGCGCTGGTCTCACTGCGGCC 135
Qy 41 HisCys 42
Db 136 CACTGC 141

RESULT 26
US-10-094-507-21
; Sequence 21, Application US/10094507
; Publication No. US20030143553A1
; GENERAL INFORMATION:
; APPLICANT: Sommer, Steve S.
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION WITH DIRECT SEQUENCING
; FILE REFERENCE: 27709-A2AA
; CURRENT APPLICATION NUMBER: US/10/094,507
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 180
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Replication segment
; NAME/KEY: CDS
; LOCATION: (1)..(180)
; OTHER INFORMATION:
US-10-094-507-21

Alignment Scores:
Pred. No.: 3,96e-05 Length: 180
Score: 117.00 Matches: 20
Percent Similarity: 56.67% Conservative: 14
Best Local Similarity: 33.33% Mismatches: 24

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Query Match: 9.30% Indels: 2
DB: 15 Gaps: 1
US-09-856-320A-2_COPY_54_282 (1-229) x US-10-094-507-21 (1-180)

QY 21 LysThrArgLeuLeuCysGlyAlaThrLeuLeuAlaProArgTrpLeuLeuThrAlaAla 40
DB 1 AAAGTTGATGCAATCTGTGGAGGCTCATCGTTAATGAAAAATGATTTAACTGCTGCC 60
QY 41 HisCysLeuLeuPro-----ArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLys 58
DB 61 CACTGTGTGAACACTGGTGTAAATACAGTTGTCAGGAGTGAACATAATATGAGGAG 120
QY 59 GluGluGlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsn 78
DB 121 ACAGAACATACAGACGAAAGCGAAATGTGATTCGAATTATTCCTCACCACCAACTACAT 180

RESULT 27
US-09-864-761-28804
; Sequence 28804, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 28804
; LENGTH: 162
; TYPE: DNA
; ORGANISM: Homo sapiens

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; FEATURE:
; OTHER INFORMATION: MAP TO AC013642.3
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.53
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.49
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.52
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.49
; OTHER INFORMATION: SWISSPROT HIT: P98064, EVALUE 8.00e-14
; OTHER INFORMATION: EST HUMAN HIT: U77054.1, EVALUE 6.00e-47
; OTHER INFORMATION: NT HIT: X59958.1, EVALUE 6.00e-03
US-09-864-761-28804

Alignment Scores:
Pred. No.: 5,98e-05 Length: 162
Score: 115.00 Matches: 26
Percent Similarity: 60.42% Conservative: 3
Best Local Similarity: 54.17% Mismatches: 13
Query Match: 9.14% Indels: 6
DB: 9 Gaps: 2

US-09-856-320A-2_COPY_54_282 (1-229) x US-09-864-761-28804 (1-162)

QY 180 GlyAspSerGlyGlyProLeuValCysAsnGln-----SerLeuGlnGly 194
DB 1 GGTGATTCGGGGACCTTTAGTCACAGGATCTGAAAGATACGTGGTATCTCATTGGA 60
QY 195 IleIleSerTrpGlyGlnAspProCysAlaIleThrArgLysProGlyValThrLys 214
DB 61 ATTGTAAGCTGGGGA---GATAACTGTGTCAAAGGACAAGCTGGAGTCTACACAA 117
QY 215 ValCysLysTyrValAspTrpIle 222
DB 118 GTGACTTATTACCGAAACTGGATT 141

RESULT 28
US-10-060-036-3294/c
; Sequence 3294, Application US/10060036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yugu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060,036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3294
; LENGTH: 184
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-036-3294

Alignment Scores:
Pred. No.: 9.43e-05 Length: 184
Score: 114.00 Matches: 24
Percent Similarity: 61.02% Conservative: 12
Best Local Similarity: 40.68% Mismatches: 17
Query Match: 9.06% Indels: 6
DB: 15 Gaps: 3

US-09-856-320A-2_COPY_54_282 (1-229) x US-10-060-036-3294 (1-184)

QY 1 IleIleLysGlyPheGluCysLysProHisSerGlnProTrpGlnAlaLeu---Phe 19
DB 178 GTTGTCATGTTGAGGATCGGCTCCCTACAGCTGGCCTGGCAGTTTCCCTGCAGTAT 119
QY 20 GluLysThrArgLeuLeu-----CysGlyAlaThrLeuLeuAlaProArgTrpLeu 36
DB 178 GTTGTCATGTTGAGGATCGGCTCCCTACAGCTGGCCTGGCAGTTTCCCTGCAGTAT 119

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Db 118 GAGAAAGTGAAGCTTCTACACACGTGTGGCGGTAGCTCTCATCGCCCGGACTGGGTT 59
Qy 37 LeuThrAlaAlaHisCysLeuLysPro-----ArgTyrIleValHisLeuGlyGln 53
Db 58 GTGACTGCGCGCACTGCATCTCGAGCTCTCGACCTTCCGACCTACAGGTGGTGTGGGCGAG 2

RESULT 29
US-10-060-036-3490
; Sequence 3490, Application US/10060036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yugu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060,036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 3490
; LENGTH: 195
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-036-3490

Alignment Scores:
Pred. No.: 0.000102 Length: 195
Score: 114.00 Matches: 24
Percent Similarity: 61.02% Conservative: 12
Best Local Similarity: 40.68% Mismatches: 17
Query Match: 9.06% Indels: 6
DB: 15 Gaps: 3

US-09-856-320A-2_COPY_54_282 (1-229) x US-10-060-036-3490 (1-195)
Qy 1 llelleLysGlyPheGluCysLysProHisSerGlnProTrpGlnAlaAlaLeu---Phe 19
Db 18 GTTGTCAATGGTGAGGATCGGTCGCCCTACAGCTGGCCCTGGCAGGTTTCCCTGCAGTAT 77
Qy 20 GluLysThrArgLeuLeu-----CysGlyAlaThrLeuIleAlaProArgTrpLeu 36
Db 78 GAGAAAGTGAAGCTTCTACACACGTGTGGCGGTAGCTCTATCGCCCGGACTGGGTT 137
Qy 37 LeuThrAlaAlaHisCysLeuLysPro-----ArgTyrIleValHisLeuGlyGln 53
Db 138 GTGACTGCGCGCACTGCATCTCGAGCTCTCGACCTACAGGTGGTGTGGGTGAG 194

RESULT 30
US-10-060-036-3865
; Sequence 3865, Application US/10060036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yugu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060,036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 3865
; LENGTH: 214
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-036-3865

Alignment Scores:
Pred. No.: 0.000116 Length: 214
Score: 114.00 Matches: 24
Percent Similarity: 61.02% Conservative: 12
Best Local Similarity: 40.68% Mismatches: 17
Query Match: 9.06% Indels: 6
DB: 15 Gaps: 3

US-09-856-320A-2_COPY_54_282 (1-229) x US-10-060-036-3865 (1-214)
Qy 1 llelleLysGlyPheGluCysLysProHisSerGlnProTrpGlnAlaAlaLeu---Phe 19
Db 37 GTTGTCAATGGTGAGGATCGGTCGCCCTACAGCTGGCCCTGGCAGGTTTCCCTGCAGTAT 96
Qy 20 GluLysThrArgLeuLeu-----CysGlyAlaThrLeuIleAlaProArgTrpLeu 36
Db 97 GAGAAAGTGAAGCTTCTACACACGTGTGGCGGTAGCTCTATCGCCCGGACTGGGTT 156
Qy 37 LeuThrAlaAlaHisCysLeuLysPro-----ArgTyrIleValHisLeuGlyGln 53
Db 157 GTGACTGCGCGCACTGCATCTCGAGCTCTCGACCTACAGGTGGTGTGGGTGAG 213

RESULT 31
US-10-060-036-3854/C
; Sequence 3854, Application US/10060036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yugu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060,036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 3854
; LENGTH: 205
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 93
; OTHER INFORMATION: n = A,T,C or G
US-10-060-036-3854

Alignment Scores:
Pred. No.: 0.000145 Length: 205
Score: 113.00 Matches: 24
Percent Similarity: 61.02% Conservative: 12
Best Local Similarity: 40.68% Mismatches: 17
Query Match: 8.98% Indels: 6
DB: 15 Gaps: 3

US-09-856-320A-2_COPY_54_282 (1-229) x US-10-060-036-3854 (1-205)
Qy 1 llelleLysGlyPheGluCysLysProHisSerGlnProTrpGlnAlaAlaLeu---Phe 19
Db 178 GTTGTCAATGGTGAGGATCGGTCGCCCTACAGCTGGCCCTGGCAGGTTTCCCTGCAGTAT 119
Qy 20 GluLysThrArgLeuLeu-----CysGlyAlaThrLeuIleAlaProArgTrpLeu 36
Db 118 GAGAAAGTGAAGCTTCTACACACGTGTGGCGGTAGCTCTATCGCCCGGACTGGGTT 59
Qy 37 LeuThrAlaAlaHisCysLeuLysPro-----ArgTyrIleValHisLeuGlyGln 53
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QY 179 GlnGlyAspSerGlyGlyProLeuValCysAsnGlnSer-----LeuGlnGly 194
Db 1 CAGGGTGACTCAGGTGGACCTTGGTGTGCACAAAGATGACGTGGTATCAGGTTGGA 60
QY 195 IleIleSerTPGlyGlnAspProCysAlaIleThrArgLysProGlyValThrLys 214
Db 61 ATCGTGAGCTGGGATGGAC---TGGCGTCAACCAATCGGCTGGTGTCTACACCAAC 117
QY 215 Val 215
Db 118 ATC 120

RESULT 35
US-10-060-036-4110
; Sequence 4110, Application US/10060036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Datin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yugu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060,036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4110
; LENGTH: 175
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-036-4110

Alignment Scores:
Pred. No.: 0.000354 Length: 175
Score: 109.00 Matches: 24
Percent Similarity: 60.34% Conservative: 11
Best Local Similarity: 41.38% Mismatches: 17
Query Match: 8.66% Indels: 6
DB: 15 Gaps: 3

US-09-856-320A-2_COPY_54_282 (1-229) x US-10-060-036-4110 (1-175)

QY 2 IleLysGlyPheGluCysLysProHisserGlnProTrpGlnAlaAlaLeu---PheGlu 20
Db 1 GTCCATGGTGAGATGCGGTCCCTACACAGCTGCGCTGCGAGTTTCCCTGCAGTATGAG 60
QY 21 LysThrArgLeuLeu-----CysGlyAlaThrLeuIleAlaProArgTrpLeuLeu 37
Db 61 AAAAGTGAAGCTTCTACACACAGTGTGGCGGTAGCTCATCGCCCGCGANTGGGTTGTG 120
QY 38 ThrAlaAlaHisCysLeuLysPro-----ArgTyrIleValHisLeuGlyGln 53
Db 121 ACTGCGGCGCACTGCATCTCGAGGGATGTGACCTACCAAGTGGTGTGGGTGAG 174

RESULT 36
US-10-060-036-3468
; Sequence 3468, Application US/10060036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Datin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yugu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060,036
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; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3468
; LENGTH: 218
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-036-3468

Alignment Scores:
Pred. No.: 0.000481 Length: 218
Score: 109.00 Matches: 20
Percent Similarity: 65.96% Conservative: 11
Best Local Similarity: 42.55% Mismatches: 12
Query Match: 8.66% Indels: 4
DB: 15 Gaps: 2

US-09-856-320A-2_COPY_54_282 (1-229) x US-10-060-036-3468 (1-218)

QY 1 IleIleLysGlyPheGluCysLysProHisserGlnProTrpGlnAlaAlaLeu---Phe 19
Db 77 GTTGTCATGGTGAGATGCGGTCCCTACACAGTGGCGCTGCGAGTTTCCCTGCAGTAT 136
QY 20 GluLysThrArgLeuLeu-----CysGlyAlaThrLeuIleAlaProArgTrpLeu 36
Db 137 GAGAAAAGTGAAGCTTCTACACACAGTGTGGCGGTAGCTCATCGCCCGCGATTGGGT 196
QY 37 LeuThrAlaAlaHisCysLeu 43
Db 197 GTGACTGCGCGCCACATGCAATC 217

RESULT 37
US-09-864-761-27190
; Sequence 27190, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aemica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
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; PRIOR APPLICATION NUMBER: PCT/US01/00670
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: US 60/234,667
 ; PRIOR FILING DATE: 2000-09-21
 ; PRIOR APPLICATION NUMBER: US 09/608,408
 ; PRIOR FILING DATE: 2000-06-30
 ; PRIOR APPLICATION NUMBER: US 09/774,203
 ; PRIOR FILING DATE: 2001-01-29
 ; NUMBER OF SEQ ID NOS: 49117
 ; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
 ; SEQ ID NO 27190
 ; LENGTH: 175
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURES:
 ; OTHER INFORMATION: MAP TO AL078474.2
 ; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.6
 ; OTHER INFORMATION: NT HIT: Y19139.1, EVALUE 6.00e-86
 ; OTHER INFORMATION: EST HUMAN HIT: BE737932.1, EVALUE 1.00e-85
 ; OTHER INFORMATION: SWISSPROT HIT: P98073, EVALUE 6.00e-30
 US-09-864-761-27190

Alignment Scores:
 Pred. No.: 0.000468 Length: 175
 Score: 108.00 Matches: 19
 Percent Similarity: 65.12% Conservative: 9
 Best Local Similarity: 44.19% Mismatches: 15
 Query Match: 8.59% Indels: 0
 DB: 9 Gaps: 0

US-09-856-320A-2_COPY_54_282 (1-229) x US-09-864-761-27190 (1-175)

QY 1 IlelelYsGlyPheGluCysLysProHisSerGlnProTrpGlnAlaLeuPheGlu 20
 Db 42 ATTGTCGAGAGTAATGCCAAGAGGGCGCTGCCCTGGTTCGTGATATAT 101
 QY 21 LysThrArgLeuLeuCysGlyAlaThrLeuLeuAlaProArgTrpLeuThrAla 40
 Db 102 GCGCGCGGACTGCTGCGCGGCGATCTCTGTCAGCAGTCACTGGTGTGTCGCGCA 161
 QY 41 HisCysLeu 43
 Db 162 CACTGCGTG 170

RESULT 38
 US-09-923-779-118
 ; Sequence 118, Application US/09923779
 ; Patent No. US20020076721A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pyle, Ruth A.
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Kalos, Michael D.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; FILE REFERENCE: 210121.553
 ; CURRENT APPLICATION NUMBER: US/09/923,779
 ; CURRENT FILING DATE: 2001-08-06
 ; NUMBER OF SEQ ID NOS: 155
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 118
 ; LENGTH: 220
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-923-779-118

Alignment Scores:
 Pred. No.: 0.000644 Length: 220
 Score: 108.00 Matches: 20
 Percent Similarity: 65.22% Conservative: 10
 Best Local Similarity: 43.48% Mismatches: 12
 Query Match: 8.59% Indels: 4
 DB: 9 Gaps: 2

US-09-856-320A-2_COPY_54_282 (1-229) x US-09-923-779-118 (1-220)
 QY 1 IlelelYsGlyPheGluCysLysProHisSerGlnProTrpGlnAlaLeu---Phe 19
 Db 81 GTTGCAATGGTGAGGATGGCGTCCCTACAGCTGGCCCTGGCAGGTTTCCCTGCAGTAT 140
 QY 20 GlulysThrArgLeuLeu-----CysGlyAlaThrLeuLeuAlaProArgTrpLeu 36
 Db 141 GAGAAAGTGGAAAGCTTCTACACACAGCTGTGGCGGTAGCCTCATCGCCCGGATTGGTT 200
 QY 37 LeuThrAlaAlaHisCys 42
 Db 201 GTGACTCGCGGCCACTGC 218

RESULT 39
 US-09-923-779-119/c
 ; Sequence 119, Application US/09923779
 ; Patent No. US20020076721A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pyle, Ruth A.
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Kalos, Michael D.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; FILE REFERENCE: 210121.553
 ; CURRENT APPLICATION NUMBER: US/09/923,779
 ; CURRENT FILING DATE: 2001-08-06
 ; NUMBER OF SEQ ID NOS: 155
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 119
 ; LENGTH: 220
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-923-779-119

Alignment Scores:
 Pred. No.: 0.000644 Length: 220
 Score: 108.00 Matches: 20
 Percent Similarity: 65.22% Conservative: 10
 Best Local Similarity: 43.48% Mismatches: 12
 Query Match: 8.59% Indels: 4
 DB: 9 Gaps: 2

US-09-856-320A-2_COPY_54_282 (1-229) x US-09-923-779-119 (1-220)
 QY 1 IlelelYsGlyPheGluCysLysProHisSerGlnProTrpGlnAlaLeu---Phe 19
 Db 140 GTTGCAATGGTGAGGATGGCGTCCCTACAGCTGGCCCTGGCAGGTTTCCCTGCAGTAT 81
 QY 20 GlulysThrArgLeuLeu-----CysGlyAlaThrLeuLeuAlaProArgTrpLeu 36
 Db 80 GAGAAAGTGGAAAGCTTCTACACACAGCTGTGGCGGTAGCCTCATCGCCCGGATTGGTT 21
 QY 37 LeuThrAlaAlaHisCys 42
 Db 201 GTGACTCGCGGCCACTGC 3

RESULT 40
 US-09-923-779-124
 ; Sequence 124, Application US/09923779
 ; Patent No. US20020076721A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pyle, Ruth A.
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Kalos, Michael D.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; FILE REFERENCE: 210121.553
 ; CURRENT APPLICATION NUMBER: US/09/923,779
 ; CURRENT FILING DATE: 2001-08-06
 ; NUMBER OF SEQ ID NOS: 155
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 124

```
; LENGTH: 220
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-923-779-124

Alignment Scores:
Pred. No.: 0.000644 Length: 220
Score: 108.00 Matches: 20
Percent Similarity: 65.22% Conservative: 10
Best Local Similarity: 43.48% Mismatches: 12
Query Match: 8.59% Indels: 4
DB: 9 Gaps: 2

US-09-856-320A-2_COPY_54_282 (1-229) x US-09-923-779-124 (1-220)
QY 1 llelellysglyphecylsProHisserGlnProTrpGlnAlaLeu---Phe 19
Db 81 GTTGTCATGTGGAGGATGCGGTCCCTACAGTCGGCGGTTCCTCGCAGTAT 140
QY 20 GluLysThrArgLeuLeu-----CysGlyAlaThrLeuLeAlaProArgTrpLeu 36
Db 141 GAGAAAGTGGAGCTTCTACACACAGTGTGGCGGTAGCCTCATCGCCCGGATTGGTT 200
QY 37 LeuThrAlaAlaHisCys 42
Db 201 GTGACTGCGGCCACTGC 218

RESULT 41
US-09-923-779-125/c
; Sequence 125, Application US/09923779
; Patent No. US20020076721A1
; GENERAL INFORMATION:
; APPLICANT: Pyle, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.553
; CURRENT APPLICATION NUMBER: US/09/923,779
; CURRENT FILING DATE: 2001-08-06
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 125
; LENGTH: 220
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-923-779-125

Alignment Scores:
Pred. No.: 0.000644 Length: 220
Score: 108.00 Matches: 20
Percent Similarity: 65.22% Conservative: 10
Best Local Similarity: 43.48% Mismatches: 12
Query Match: 8.59% Indels: 4
DB: 9 Gaps: 2

US-09-856-320A-2_COPY_54_282 (1-229) x US-09-923-779-125 (1-220)
QY 1 llelellysglyphecylsProHisserGlnProTrpGlnAlaLeu---Phe 19
Db 140 GTTGTCATGTGGAGGATGCGGTCCCTACAGTCGGCGGTTCCTCGCAGTAT 81
QY 20 GluLysThrArgLeuLeu-----CysGlyAlaThrLeuLeAlaProArgTrpLeu 36
Db 80 GAGAAAGTGGAGCTTCTACACACAGTGTGGCGGTAGCCTCATCGCCCGGATTGGTT 21
QY 37 LeuThrAlaAlaHisCys 42
Db 201 GTGACTGCGGCCACTGC 3

RESULT 42
US-09-923-779-126
; Sequence 126, Application US/09923779
; Patent No. US20020076721A1
; GENERAL INFORMATION:
; APPLICANT: Pyle, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.553
; CURRENT APPLICATION NUMBER: US/09/923,779
; CURRENT FILING DATE: 2001-08-06
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126
; LENGTH: 220
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-923-779-126

Alignment Scores:
Pred. No.: 0.000644 Length: 220
Score: 108.00 Matches: 20
Percent Similarity: 65.22% Conservative: 10
Best Local Similarity: 43.48% Mismatches: 12
Query Match: 8.59% Indels: 4
DB: 9 Gaps: 2

US-09-856-320A-2_COPY_54_282 (1-229) x US-09-923-779-126 (1-220)
QY 1 llelellysglyphecylsProHisserGlnProTrpGlnAlaLeu---Phe 19
Db 81 GTTGTCATGTGGAGGATGCGGTCCCTACAGTCGGCGGTTCCTCGCAGTAT 140
QY 20 GluLysThrArgLeuLeu-----CysGlyAlaThrLeuLeAlaProArgTrpLeu 36
Db 141 GAGAAAGTGGAGCTTCTACACACAGTGTGGCGGTAGCCTCATCGCCCGGATTGGTT 200
QY 37 LeuThrAlaAlaHisCys 42
Db 201 GTGACTGCGGCCACTGC 218

RESULT 43
US-09-923-779-127/c
; Sequence 127, Application US/09923779
; Patent No. US20020076721A1
; GENERAL INFORMATION:
; APPLICANT: Pyle, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.553
; CURRENT APPLICATION NUMBER: US/09/923,779
; CURRENT FILING DATE: 2001-08-06
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 127
; LENGTH: 220
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-923-779-127

Alignment Scores:
Pred. No.: 0.000644 Length: 220
Score: 108.00 Matches: 20
Percent Similarity: 65.22% Conservative: 10
Best Local Similarity: 43.48% Mismatches: 12
Query Match: 8.59% Indels: 4
DB: 9 Gaps: 2

US-09-856-320A-2_COPY_54_282 (1-229) x US-09-923-779-127 (1-220)
QY 1 llelellysglyphecylsProHisserGlnProTrpGlnAlaLeu---Phe 19
Db 81 GTTGTCATGTGGAGGATGCGGTCCCTACAGTCGGCGGTTCCTCGCAGTAT 140
QY 20 GluLysThrArgLeuLeu-----CysGlyAlaThrLeuLeAlaProArgTrpLeu 36
Db 141 GAGAAAGTGGAGCTTCTACACACAGTGTGGCGGTAGCCTCATCGCCCGGATTGGTT 200
QY 37 LeuThrAlaAlaHisCys 42
Db 201 GTGACTGCGGCCACTGC 218
```

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Db 140 GTTCTCAATGGTGGAGGATGGCGTCCCTACAGCTGGCCCTGGCAGGTTCCCTCGCAGTAT 81
Qy 20 GlulysThrArgLeuLeu-----CysGlyAlaThrLeuIleAlaProArgTrrpLeu 36
Db 80 GAGAAAGTGAAGCTTCTACACACAGTGTGGCGGTAGCTTCATCGCCCGGATGGGTT 21
Qy 37 LeuThrAlaAlaHisCys 42
Db 20 GTGACTCGCGCCACTGC 3

RESULT 44
US-10-029-386-14818/c
; Sequence 14818, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; FILE REFERENCE: AEMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 14818
; LENGTH: 176
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR21 61.0
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.4
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.89
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.95
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.4
; OTHER INFORMATION: NT HIT: AL163285.2, EVALUE 1.00e-94
; OTHER INFORMATION: SWISSPROT HIT: O15393, EVALUE 1.00e-26
; OTHER INFORMATION: EST_HUMAN HIT: AA457407.1, EVALUE 7.00e-85
US-10-029-386-14818

Alignment Scores:
Pred. No.: 0.000543 Length: 176
Score: 107.50 Matches: 24
Percent Similarity: 57.69% Conservative: 6
Best Local Similarity: 46.15% Mismatches: 17
Query Match: 8.55% Indels: 5
DB: 15 Gaps: 2

US-09-856-320A-2_COPY_54_282 (1-229) x US-10-029-386-14818 (1-176)
Qy 180 GlyAspSerGlyGlyProLeuValCysAsnGlnSer-----LeuGlnGlyIle 195
Db 176 GGTGACAGTGGAGGGCTCTGGTCATCTCGAAGAACAAATATCTGGTGGCTGATAGGGAT 117
Qy 196 IleSerTrpGlyGlnAspProCysAlaIleThrArgLysProGlyValThrLysVal 215
Db 116 ACAAGCTGGGGTCTTCGCG---TGTCGCAAGCTTACAGACAGGAGGTGTACGGGAATGTG 60
Qy 216 CysLysTyrValAspTrpIleGlnGluThrMetLys 227
Db 59 ATGGTATTCACGAGCTGGATTTATCGACAAATGAGG 24

RESULT 45
US-10-029-386-26680
; Sequence 26680, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; FILE REFERENCE: AEMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 14818
; LENGTH: 176
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR21 61.0
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.4
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.89
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.95
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.4
; OTHER INFORMATION: NT HIT: AL163285.2, EVALUE 1.00e-94
; OTHER INFORMATION: SWISSPROT HIT: O15393, EVALUE 1.00e-26
; OTHER INFORMATION: EST_HUMAN HIT: AA457407.1, EVALUE 7.00e-85
US-10-029-386-14818

Alignment Scores:
Pred. No.: 0.000543 Length: 176
Score: 107.50 Matches: 24
Percent Similarity: 57.69% Conservative: 6
Best Local Similarity: 46.15% Mismatches: 17
Query Match: 8.55% Indels: 5
DB: 15 Gaps: 2

US-09-856-320A-2_COPY_54_282 (1-229) x US-10-029-386-14818 (1-176)
Qy 180 GlyAspSerGlyGlyProLeuValCysAsnGlnSer-----LeuGlnGlyIle 195
Db 176 GGTGACAGTGGAGGGCTCTGGTCATCTCGAAGAACAAATATCTGGTGGCTGATAGGGAT 117
Qy 196 IleSerTrpGlyGlnAspProCysAlaIleThrArgLysProGlyValThrLysVal 215
Db 116 ACAAGCTGGGGTCTTCGCG---TGTCGCAAGCTTACAGACAGGAGGTGTACGGGAATGTG 60
Qy 216 CysLysTyrValAspTrpIleGlnGluThrMetLys 227
Db 59 ATGGTATTCACGAGCTGGATTTATCGACAAATGAGG 24

RESULT 46
US-09-923-779-89
; Sequence 89, Application US/09923779
; Patent No. US20020076721A1
; GENERAL INFORMATION:
; APPLICANT: Pyle, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.553
; CURRENT APPLICATION NUMBER: US/09/923,779
; CURRENT FILING DATE: 2001-08-06
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 208
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 48, 49
; OTHER INFORMATION: n = A,T,C or G
US-09-923-779-89

Alignment Scores:
Pred. No.: 0.000787 Length: 208
Score: 107.00 Matches: 20
Percent Similarity: 65.22% Conservative: 10
Best Local Similarity: 43.48% Mismatches: 12
Query Match: 8.51% Indels: 4
DB: 9 Gaps: 2

US-09-856-320A-2_COPY_54_282 (1-229) x US-09-923-779-89 (1-208)
Qy 142 CysAlaAsnIleThrIleIleGluHisGlnCysGluAsnAlaTyrProGlyAsnIle 161
Db 3 TGCTGTGATGCTCGGTGCTGACCCAGGCTGAGTGTAAAGCTCTTACCTCGAAAGATT 62
Qy 162 ThrAspThrMetValCysAlaSerValGlnGluGlyLysAspSerCysGln 179
Db 63 ACCAACAGCATGTTCTGTGTGGGCTTCTTGAGGGAGGCAAGGATTCCTGCCAG 116

RESULT 46
US-09-923-779-89
; Sequence 89, Application US/09923779
; Patent No. US20020076721A1
; GENERAL INFORMATION:
; APPLICANT: Pyle, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.553
; CURRENT APPLICATION NUMBER: US/09/923,779
; CURRENT FILING DATE: 2001-08-06
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 208
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 48, 49
; OTHER INFORMATION: n = A,T,C or G
US-09-923-779-89

Alignment Scores:
Pred. No.: 0.000357 Length: 118
Score: 107.00 Matches: 17
Percent Similarity: 65.79% Conservative: 8
Best Local Similarity: 44.74% Mismatches: 13
Query Match: 8.51% Indels: 0
DB: 15 Gaps: 0

US-09-856-320A-2_COPY_54_282 (1-229) x US-10-029-386-26680 (1-118)
Qy 142 CysAlaAsnIleThrIleIleGluHisGlnCysGluAsnAlaTyrProGlyAsnIle 161
Db 3 TGCTGTGATGCTCGGTGCTGACCCAGGCTGAGTGTAAAGCTCTTACCTCGAAAGATT 62
Qy 162 ThrAspThrMetValCysAlaSerValGlnGluGlyLysAspSerCysGln 179
Db 63 ACCAACAGCATGTTCTGTGTGGGCTTCTTGAGGGAGGCAAGGATTCCTGCCAG 116

RESULT 46
US-09-923-779-89
; Sequence 89, Application US/09923779
; Patent No. US20020076721A1
; GENERAL INFORMATION:
; APPLICANT: Pyle, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.553
; CURRENT APPLICATION NUMBER: US/09/923,779
; CURRENT FILING DATE: 2001-08-06
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 208
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 48, 49
; OTHER INFORMATION: n = A,T,C or G
US-09-923-779-89

Alignment Scores:
Pred. No.: 0.000357 Length: 118
Score: 107.00 Matches: 17
Percent Similarity: 65.79% Conservative: 8
Best Local Similarity: 44.74% Mismatches: 13
Query Match: 8.51% Indels: 0
DB: 15 Gaps: 0

US-10-029-386-26680
; Sequence 26680, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; FILE REFERENCE: AEMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 14818
; LENGTH: 176
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR9.3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.64
; OTHER INFORMATION: EST_HUMAN HIT: BE045793.1, EVALUE 7.00e-59
; OTHER INFORMATION: NT HIT: GI14742065, EVALUE 3.00e-60
; OTHER INFORMATION: SWISSPROT HIT: P35030, EVALUE 1.00e-17
US-10-029-386-26680
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Db 94 ACGRGTGGCGGTAGCCTCATCGCCCGCGATTGGTTGTGACTGCGCGCCACTGCATCTCG 35

Qy 45 Pro-----ArgTyrIleValHisLeuGlyGln 53

Db 34 AGGATCTGACCTACCAAGGTGGTGTGGGTGAG 2

RESULT 50

US-10-424-599-75219

; Sequence 75219, Application US/10424599

; Publication No. US20040031072A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J

; APPLICANT: Kovalic David K

; APPLICANT: Zhou Yihua

; APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53223)B

; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684

; SEQ ID NO 75219

; LENGTH: 189

; TYPE: DNA

; ORGANISM: Glycine max

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT3847_38936C.1

US-10-424-599-75219

Alignment Scores:

Pred. No.:	0.00183	Length:	189
Score:	103.50	Matches:	26
Percent Similarity:	47.69%	Conservative:	5
Best Local Similarity:	40.00%	Mismatches:	25
Query Match:	8.23%	Indels:	9
DB:	13	Gaps:	2

US-09-856-320A-2_COPY_54_282 (1-229) x US-10-424-599-75219 (1-189)

Qy 162 ThrAspThrMetValCysAlaSerValGlnGluGlyLysAspSerCysGlnGlyAsp 181

Db 2 TCTCAAAACATGTTCTGTGTGGACCCCATCTCTAAAGCAGGACGCTGCCAGGGGGAT 61

Qy 182 SerGlyGly-----ProLeuValCysAsnGlnSerLeuGlnGlyIle 195

Db 62 AGTGGGGCGTTTGTGAGTAAGGACCCGAACTGATCGTGGGTGGCCACGGGCATC 121

Qy 196 IleSerTrpGlyGlnAspProCysAlaIleThrArgLysProGlyValTyrThrLysVal 215

Db 122 GTGTCCTGGGGC-----ATCGGGTGCAGCAGGGGGCTATGGCTTCTACCAAAAGTG 172

Qy 216 CysLysTyrValAsp 220

Db 173 CTCAACTACGTGGAC 187

Search completed: June 27, 2004, 00:33:00

Job time : 476 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 26, 2004, 23:38:31 ; Search time 434 Seconds
(without alignments)
2241.561 Million cell updates/sec

Title: US-09-856-320A-2_COPY_54_282

Perfect score: 1258
Sequence: 1 IIKGFECKPHSQPQAALFE.....GVYTKVCKYVDWIOETMKN 229

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 3849990

Minimum DB seq length: 0

Maximum DB seq length: 229

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-O=/cpn2_1/USPTO.spool/US09856320/runat_25062004_124554_1052/app_query.fasta_1.391
-DB=N_Geneseq_23Jan04 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -STAR=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=500 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MTN=0 -ALIGN=50
-MODE=LOCAL -OUTFMT=ptc -NORV=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=229
-USER=US09856320 @CNC 1 1 470 @runat_25062004_124554_1052 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FCGAPOP=6
-FCGAPEXT=7 -XGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_29Jan04.*

1: Geneseqn1980s.*
2: Geneseqn1990s.*
3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
6: Geneseqn2002s.*
7: Geneseqn2003as.*
8: Geneseqn2003bs.*
9: Geneseqn2003cs.*
10: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	ID	Description
1	206	16.4	153	6	Abk48915 Novel hum
2	202.5	16.1	205	4	Aa24516 Human ova
3	194	15.4	178	7	ADA05697 Human NOV
4	188	14.9	198	3	Aa295014 Prostate
5	187	14.9	220	6	ABN17410 Human ORF
6	169	13.4	196	5	ABV33773 Human pro
7	169	13.4	196	5	ABV42670 Human pro
8	168	13.4	200	2	AAV60379 mRNA targ

9	164	13.0	154	6	ABK48905	Novel hum
10	163	13.0	216	6	ABK30236	Human G-p
11	163.5	13.0	202	6	ABN89908	Mouse cto
12	150	11.9	207	2	AAT40842	Serine pr
13	150	11.9	207	4	AAC90850	Flea seri
14	149.5	11.9	203	7	ABX46133	Bovine ES
15	147	11.7	208	2	AAT92975	CDNA for
16	147	11.7	225	2	AAT40854	Serine pr
17	147	11.7	225	2	AAV04599	Flea seri
18	147	11.7	225	4	AAC90862	Flea seri
19	146	11.6	218	2	AAT40847	Serine pr
20	146	11.6	218	2	AAV04590	Flea seri
21	146	11.6	218	4	AAC90855	Flea seri
22	136	10.8	137	6	ABK48911	Novel hum
23	136	10.8	153	6	ABL80256	Human ova
24	135	10.7	285	2	AAQ31930	Human scu
25	134.5	10.7	227	2	AAV57985	Human BS2
26	132	10.5	180	3	AAZ89009	Rat Facto
27	131	10.4	180	3	AAZ89011	Rabbit Fa
28	130	10.3	180	3	AAZ89008	Murine Fa
29	128	10.2	180	3	AAZ89010	Cavea sp.
30	127	10.1	176	5	ABV38446	Human pro
31	123.5	9.8	159	6	ABK30380	Human G-p
32	123	9.8	178	6	ABA92483	DNA oligo
33	123	9.8	178	6	ABA01120	Human PSA
34	123	9.8	178	6	ABS52622	Human DNA
35	123	9.8	178	7	ABZ59354	Loop-medi
36	121	9.6	180	3	AAZ89012	Sheep Fac
37	120.5	9.6	179	5	ABV38147	Human pro
38	120.5	9.6	179	5	ABV44351	Human pro
39	117	9.3	172	8	AAD58752	Human tra
40	117	9.3	180	3	AAZ89007	Human tra
41	116	9.2	172	8	AAD58758	Human tra
42	115	9.1	162	4	AAI53283	Probe #21
43	115	9.1	162	4	AAK47449	Human bon
44	115	9.1	162	4	AAK21293	Human bra
45	114	9.1	184	6	ABV97886	Human liv
46	114	9.1	184	6	ABV97886	Human pan
47	114	9.1	195	6	ABV98082	Human pan
48	114	9.1	214	6	ABV98457	Human pan
49	113	9.0	94	3	AAA64312	PCR pimer
50	113	9.0	205	6	ABV98446	Human pan
51	113	9.0	222	4	AAD14836	Human pan
52	112	8.9	181	6	ABV98390	Human pan
53	111.5	8.9	93	3	AAA64311	PCR pimer
54	109	8.7	175	6	ABV98702	Human pan
55	109	8.7	218	6	ABV98060	Human pan
56	108	8.6	175	4	AAK17832	Human bra
57	108	8.6	220	6	ABK44185	CDNA #125
58	108	8.6	220	6	ABK44184	CDNA #124
59	108	8.6	220	6	ABK44186	CDNA #126
60	108	8.6	220	6	ABK44178	CDNA #118
61	108	8.6	220	6	ABK44179	CDNA #119
62	108	8.6	220	6	ABK44179	CDNA #119
63	107	8.5	208	6	ABK44149	CDNA #89
64	105.5	8.4	192	2	AAT40841	Serine pr
65	105.5	8.4	192	4	AAC90849	Flea seri
66	105	8.3	156	6	ABV98175	Human pan
67	104.5	8.3	138	6	ABK31801	DNA encod
68	104	8.3	157	6	ABV97961	Human pan
69	103	8.2	226	2	AAQ33009	Human scu
70	101.5	8.1	116	4	AAI20964	Probe #10
71	101.5	8.1	116	4	ABK66033	Human foe
72	101.5	8.1	116	4	AAI46211	Probe #14
73	101.5	8.1	116	4	ABK48157	Human bre
74	101.5	8.1	116	4	ABA33118	Probe #11
75	101.5	8.1	116	4	AAK40196	Human bon
76	101.5	8.1	116	4	AAK14457	Human bra
77	101.5	8.1	116	4	ABV339776	Human liv
78	101.5	8.1	116	5	AAI06677	Probe #66
79	101.5	8.1	116	5	ABV33773	Human pro
80	101	8.0	216	6	ABK30257	Human G-p
81	101	8.0	224	7	ABV74948	Nucleotid

82	99	7.9	162	8	AAD58766	Human tra	155	80	6.4	200	6	AAD37038	Targettin
83	98.5	7.8	155	2	AAT13998	Mouse p6-	156	79	6.3	142	6	ABL63338	Breast ca
84	98.5	7.8	155	2	AAT31747	L37 conse	157	79	6.3	142	6	ABL65239	Lung canc
85	98.5	7.8	155	3	AAAS2250	Mouse pre	158	79	6.3	142	6	ABL64712	Lung canc
86	98.5	7.8	155	3	AAAS9705	Mouse bod	159	79	6.3	142	6	ABL62036	Colon ade
87	98.5	7.8	155	8	ACD13607	Mouse cdn	160	79	6.3	142	6	ABL68304	Lung canc
88	98.5	7.8	197	6	ABKJ5330	Human air	c 161	79	6.3	181	6	ABK16733	Epithelin
89	98	7.8	177	2	AQAG3787	Bovine tr	162	79	6.3	186	2	AAT40826	Serine pr
90	98	7.8	211	6	ABK44076	cdNA #16	163	79	6.3	186	4	AAC90831	Flea seri
91	96	7.6	65	6	ABN53102	Mouse spl	164	78	6.2	61	6	ABQ78140	Synthetic
92	95.5	7.6	155	2	AAAO3776	Mouse p6-	165	78	6.2	168	2	AAT40827	Serine pr
93	95.5	7.6	155	3	AAAS9706	Mouse p6-	166	78	6.2	168	2	AAC90832	Flea seri
94	95.5	7.6	155	8	ACD13608	Mouse p6-	167	77.5	6.2	159	2	AAT40823	Serine pr
95	95.5	7.6	168	6	AAD58763	Human tra	168	77.5	6.2	159	4	AAC90828	Flea seri
96	95	7.6	90	6	ABQ78147	Synthetic	c 169	77	6.1	96	3	AAA64304	PCR pimer
97	95	7.6	168	2	AAT40824	Serine pr	170	76.5	6.1	124	6	AAD29820	Human EST
98	95	7.6	168	4	AAC90829	Flea seri	171	76	6.0	63	2	AAT58862	Oligomer
99	95	7.6	172	4	ABA73267	Human foe	172	76	6.0	65	6	ABN28524	Rat splc
100	95	7.6	172	4	ABA72552	Human foe	173	76	6.0	65	6	ABN28537	Rat splc
101	95	7.6	172	4	AAI52965	Probe #21	174	76	6.0	65	6	ABN53099	Mouse spl
102	95	7.6	172	4	AAK47129	Human bon	c 175	76	6.0	200	3	AAA64308	PCR pimer
103	95	7.6	172	4	AAK47869	Human bon	176	76	6.0	200	7	AAD48774	3' target
104	95	7.6	172	4	AAK20976	Human bra	c 177	76	6.0	227	6	ABV98147	Human pan
105	95	7.6	172	4	AAK31703	Human bra	c 178	75.5	6.0	156	4	AAAL26333	Human bre
106	95	7.6	172	4	ABSA47587	Human liv	c 179	75.5	6.0	168	4	AAAL19283	Human bre
107	93	7.4	137	8	AAD58760	Human tra	180	75.5	6.0	217	4	AAAL19398	Human bre
108	92.5	7.4	219	4	AAAF4532	Mouse dex	181	75	6.0	69	8	ACC85430	Chymotryp
109	92	7.3	60	6	ABN35820	Human spl	c 182	75	6.0	80	2	AAAX23293	TR1 PCR
110	92	7.3	134	6	ABA90277	Human ORF	c 183	75	6.0	127	3	AAC93911	Cat flea
111	92	7.3	162	2	AAT40829	Serine pr	184	75	6.0	164	4	AAAL19327	Human bre
112	92	7.3	162	2	AAV04592	Flea seri	185	74	5.9	61	2	AAAX52453	Reverse p
113	92	7.3	162	4	AAC90834	Flea seri	186	74	5.9	61	3	AAA46916	PCR prime
114	91	7.2	90	2	AAVS8593	Prostate	187	74	5.9	61	3	ADC78594	Human PRO
115	91	7.2	90	2	AAV61208	cdNA sequ	188	74	5.9	61	4	AAF72611	Human PRO
116	91	7.2	90	3	AAA06356	Human inm	189	74	5.9	61	7	ACA59129	Human PRO
117	91	7.2	90	3	ABS71261	Human pro	190	74	5.9	61	7	ACA58526	PCR prime
118	91	7.2	90	4	AAH93472	Human pro	191	74	5.9	61	7	ACA60233	Human sec
119	91	7.2	90	4	AAAG3564	Human pro	192	74	5.9	61	7	ACD07633	Novel hum
120	91	7.2	90	4	AAH02537	Prostate	193	74	5.9	61	7	ABX71681	Human sec
121	91	7.2	90	4	AAH84786	Human pro	194	74	5.9	61	7	ACH07013	Human sec
122	91	7.2	90	5	ACAS9373	Prostate	195	74	5.9	61	7	ABX96250	Human sec
123	91	7.2	90	5	AAAS10115	Human pro	196	74	5.9	61	7	ACA05571	Human sec
124	91	7.2	90	6	ABL94936	Human P10	197	74	5.9	61	7	ACD20238	Human sec
125	91	7.2	90	6	ABSS58645	Prostate	198	74	5.9	61	7	ACA55041	Novel sec
126	91	7.2	90	7	ACC95100	Prostate	199	74	5.9	61	8	ACD19876	Human sec
127	91	7.2	90	9	ADBI33570	Human pro	200	74	5.9	61	8	ADB29487	Human sec
128	90.5	7.2	200	6	ABQ75507	Murine tr	201	74	5.9	61	8	ADA18343	Human sec
129	90	7.2	57	6	ABQ78145	Synthetic	202	74	5.9	61	8	ACD67023	Human sec
130	90	7.2	147	3	AAAC93919	Cat flea	203	74	5.9	61	8	ACD83184	Human PRO
131	89	7.1	137	8	AAD58755	Human tra	204	74	5.9	61	8	ADA16318	Human sec
132	88	7.0	74	2	AAQ33790	Bovine tr	205	74	5.9	61	8	ADA42463	Human sec
133	87.5	7.0	116	2	AAQ31931	Human scu	206	74	5.9	61	8	ACD23362	Human PRO
134	87	6.9	93	2	AAQ63782	Bovine tr	207	74	5.9	61	8	ADA16742	Human sec
135	86	6.8	100	4	AAH02409	Human fac	208	74	5.9	61	8	ADA13171	Human sec
136	86	6.8	135	6	ABK31800	DNA encod	209	74	5.9	61	8	ADA42039	Human sec
137	85	6.8	60	2	AAT89214	Prostate	210	74	5.9	61	8	ADA17386	Human sec
138	85	6.8	77	2	AAQ63786	Bovine tr	211	74	5.9	61	8	ADA42889	Human sec
139	85	6.8	100	4	AAH02410	Human fac	212	74	5.9	61	8	ACD23724	Human PRO
140	85	6.8	168	2	AAT40820	Serine pr	213	74	5.9	61	8	ADB77808	Human sec
141	85	6.8	168	4	AAC90825	Flea seri	214	74	5.9	61	9	ADB74944	Human sec
142	84	6.7	137	8	AAD58765	Human tra	215	74	5.9	61	9	ADC28590	Human sec
143	84	6.7	164	5	ABV35541	Human pro	216	74	5.9	61	9	ADC3790	Human sec
144	84	6.7	193	6	ABV98322	Human pan	217	74	5.9	61	9	ADC40304	Human sec
145	83.5	6.6	200	6	AAD37041	Targettin	218	74	5.9	61	9	ADC19128	Human sec
146	83	6.6	60	6	ABQ78144	Synthetic	219	74	5.9	61	9	ADC34428	Human sec
147	83	6.6	107	5	ABV08544	Human pro	220	74	5.9	61	9	ADC29483	Human sec
148	83	6.6	137	7	ABQ83346	KLK4 alte	221	74	5.9	61	9	ADC29014	Human sec
149	83	6.6	200	6	ABD37040	Targettin	222	74	5.9	61	9	ADC40899	Human sec
150	82.5	6.6	220	6	ABK30330	Human G-p	223	74	5.9	61	9	ADC19556	Human sec
151	82	6.5	193	6	ABV97917	Human pan	224	74	5.9	61	9	ADC34004	Human sec
152	81.5	6.5	229	5	AAOS5418	Mammalian	225	74	5.9	61	9	ADC13074	Human sec
153	81	6.4	74	2	AAQ63791	Bovine tr	226	74	5.9	61	9	ADC12526	Human sec
154	80.5	6.4	76	2	AAQ63788	Bovine tr	227	74	5.9	61	9	ADD05081	Human sec

228	74	5.9	61	9	ADD04087	Abd04087 Human sec	301	60	4.8	65	6	ABN28495	Abn28495 Rat splc
229	74	5.9	61	9	ADD03663	Abd03663 Human sec	302	60	4.8	92	3	AAA64313	Aaa64313 PCR pimer
230	74	5.9	61	9	ABE34915	AbE34915 Human sec	303	60	4.8	179	3	ABL23657	AbL23657 Drosophil
231	74	5.9	61	10	ADE793360	Ade793360 Human sec	304	60	4.8	227	3	AAZ49262	Aaz49262 Human hyd
232	74	5.9	61	10	ADe79784	AdE79784 Human sec	305	60	4.8	229	2	Aaz41399	Aaz41399 Human nor
233	74	5.9	61	10	ADe73460	AdE73460 Human sec	306	59.5	4.7	119	2	AAZ52454	Aaz52454 Probe use
234	74	5.9	61	10	ADe73995	AdE73995 Human sec	307	59.5	4.7	119	3	AAA46917	Aaa46917 Probe use
C 235	74	5.9	143	4	ABA72967	AbA72967 Human foe	308	59.5	4.7	119	3	ADCF78595	AdCf78595 Human PRO
C 236	74	5.9	143	4	AAI53391	Aai53391 Probe #22	309	59.5	4.7	119	3	Aaf72612	Aaf72612 Human PRO
C 237	74	5.9	143	4	AAK47559	Aak47559 Human bon	310	59.5	4.7	119	7	ACA59130	Aca59130 Human PRO
C 238	74	5.9	143	4	AAK21398	Aak21398 Human bra	311	59.5	4.7	119	7	ACA58527	Aca58527 Probe #50
C 239	74	5.9	143	4	AS47294	AsE47294 Human liv	312	59.5	4.7	119	7	ACa60234	AcA60234 Human sec
C 240	74	5.9	143	6	AS22654	AsE22654 Human gen	313	59.5	4.7	119	7	ACD07634	AcD07634 Novel hum
C 241	74	5.9	199	4	AAI08940	Aai08940 Human bre	314	59.5	4.7	119	7	ABX71682	AbX71682 Human sec
242	73	5.8	182	6	ABT06520	AbT06520 Human ser	315	59.5	4.7	119	7	ACH07014	Ach07014 Human sec
243	73	5.8	210	1	AAAN90785	Aan90785 Sequence	316	59.5	4.7	119	7	ABX96251	AbX96251 Human sec
244	73	5.8	210	3	AAZ89014	Aaz89014 Human fac	317	59.5	4.7	119	7	ACA05572	Aca05572 Human sec
C 245	71.5	5.7	76	2	AAQ63789	Aaq63789 Bovine tr	318	59.5	4.7	119	7	ACD20239	AcD20239 Human sec
C 246	71.5	5.7	93	2	AAQ63783	Aaq63783 Bovine tr	319	59.5	4.7	119	7	ACA55042	AcA55042 Novel sec
247	71	5.6	51	4	AAI26842	Aai26842 Human SNP	320	59.5	4.7	119	8	ACD19877	AcD19877 Human sec
248	71	5.6	60	4	AAH02328	Aah02328 Human fac	321	59.5	4.7	119	8	ADB29488	AdB29488 Human sec
249	71	5.6	67	2	AAAX78020	Aax78020 Chimeric	322	59.5	4.7	119	8	ADA18344	Ada18344 Human sec
250	71	5.6	214	1	AAAT71331	Aat71331 Exon 3 hu	323	59.5	4.7	119	8	ACD67024	AcD67024 Human sec
251	68	5.4	60	6	ABN35936	Abn35936 Human spl	324	59.5	4.7	119	8	ACD83185	AcD83185 Human PRO
252	68	5.4	65	6	ABN53220	Abn53220 Mouse spl	325	59.5	4.7	119	8	ADA16319	Ada16319 Human sec
253	68	5.4	200	6	AAI44661	Aai44661 Clr gene	326	59.5	4.7	119	8	ADA42464	Ada42464 Human sec
254	67.5	5.4	159	2	AAAT40843	Aat40843 Serine pr	327	59.5	4.7	119	8	ACD23363	AcD23363 Human PRO
255	67.5	5.4	159	4	AAC90851	Aac90851 Flea seri	328	59.5	4.7	119	8	ADA16743	Ada16743 Human sec
C 256	67	5.3	36	6	AAAS20774	Aas20774 Mutagenic	329	59.5	4.7	119	8	ADA13172	Ada13172 Human sec
C 257	66.5	5.3	206	2	AAQ06663	Aaq06663 Synthetic	330	59.5	4.7	119	8	ADA42040	Ada42040 Human sec
C 258	66.5	5.3	217	2	AAQ06662	Aaq06662 Synthetic	331	59.5	4.7	119	8	ADA17387	Ada17387 Human sec
C 259	66	5.2	81	2	AAQ63777	Aaq63777 Bovine tr	332	59.5	4.7	119	8	ADA42890	Ada42890 Human sec
260	66	5.2	210	7	ACC49832	Acc49832 Human cyt	333	59.5	4.7	119	8	ACD23725	AcD23725 Human PRO
261	65.5	5.2	208	4	AAI09038	Aai09038 Human bre	334	59.5	4.7	119	9	ADB77809	AdB77809 Human sec
262	65	5.2	60	6	ABN35844	Abn35844 Human spl	335	59.5	4.7	119	9	ADB74945	AdB74945 Human sec
263	65	5.2	65	6	ABN53148	Abn53148 Mouse spl	336	59.5	4.7	119	9	ADC28591	AdC28591 Human sec
264	65	5.2	78	8	ACC85424	Acc85424 Chymotryp	337	59.5	4.7	119	9	ADC39791	AdC39791 Human sec
265	65	5.2	81	2	AAQ63776	Aaq63776 Bovine tr	338	59.5	4.7	119	9	ADC19129	AdC19129 Human sec
266	65	5.2	150	2	AAQ49769	Aaq49769 CAP37 pro	339	59.5	4.7	119	9	ADC34429	AdC34429 Human sec
267	65	5.2	156	2	AAI40819	Aai40819 Serine pr	340	59.5	4.7	119	9	ADC29484	AdC29484 Human sec
268	65	5.2	156	4	AAC90824	Aac90824 Flea seri	341	59.5	4.7	119	9	ADC29015	AdC29015 Human sec
269	65	5.2	203	4	AAC89749	Aac89749 Human gas	342	59.5	4.7	119	9	ADC40900	AdC40900 Human sec
C 270	64	5.1	91	2	AAAX78018	Aax78018 Chimeric	343	59.5	4.7	119	9	ADC19557	AdC19557 Human sec
271	64	5.1	91	2	AAAX78017	Aax78017 Chimeric	344	59.5	4.7	119	9	ADC34005	AdC34005 Human sec
272	64	5.1	120	2	AAAT40828	Aat40828 Serine pr	345	59.5	4.7	119	9	ADC13075	AdC13075 Human sec
273	64	5.1	120	4	AAC90833	Aac90833 Flea seri	346	59.5	4.7	119	9	ADC12527	AdC12527 Human sec
274	64	5.1	136	7	ACC49841	Acc49841 Human rec	347	59.5	4.7	119	9	ADD05082	AdD05082 Human sec
275	64	5.1	197	2	AAV04603	Aav04603 Flea seri	348	59.5	4.7	119	9	ADD04088	AdD04088 Human sec
276	64	5.1	197	4	AAC90894	Aac90894 Flea seri	349	59.5	4.7	119	9	ADD03664	AdD03664 Human sec
C 277	64	5.1	219	5	AAH52279	Aah52279 Human App	350	59.5	4.7	119	9	ADe34916	Ade34916 Human sec
C 278	64	5.1	220	3	AAC09574	Aac09574 Human sec	351	59.5	4.7	119	10	ADe79361	Ade79361 Human sec
C 279	63	5.0	63	2	AAAT58863	Aat58863 Oligomer	352	59.5	4.7	119	10	ADe79785	Ade79785 Human sec
C 280	63	5.0	88	2	AAQ63785	Aaq63785 Bovine tr	353	59.5	4.7	119	10	ADe73461	Ade73461 Human sec
281	62.5	5.0	72	8	ACC85431	Acc85431 Chymotryp	354	59.5	4.7	119	10	ADe73996	Ade73996 Human sec
282	62	4.9	39	2	AAV72614	Aav72614 Rat Facto	355	59.5	4.7	159	2	AAAT40825	Aat40825 Serine pr
283	62	4.9	39	2	AAZ09550	Aaz09550 Rat Facto	356	59.5	4.7	159	4	AAC90830	Aac90830 Flea seri
284	62	4.9	88	2	AAQ63784	Aaq63784 Bovine tr	357	59.5	4.7	168	6	ABN16422	Abn16422 Human ORF
285	62	4.9	100	3	AAAE4309	Aae4309 PCR pimer	358	59.5	4.7	177	6	AAAT40821	Aat40821 Serine pr
286	61.5	4.9	135	7	ACC49844	Acc49844 Human rec	359	59.5	4.7	177	4	AAC90826	Aac90826 Flea seri
287	61	4.8	60	6	ABN35858	Abn35858 Human spl	360	59.5	4.7	200	6	AAI44656	Aai44656 UbiQuitin
288	61	4.8	65	6	ABN28522	Abn28522 Rat splc	361	59	4.7	39	4	AAAF29713	Aaf29713 Murine fa
289	61	4.8	65	6	ABN53110	Abn53110 Mouse spl	362	59	4.7	39	4	AAAF29712	Aaf29712 Murine fa
290	61	4.8	152	2	AAAX10848	Aax10848 Human bia	363	59	4.7	43	3	AAA37221	Aaa37221 Human PRO
C 291	61	4.8	206	4	AAK53895	Aak53895 Murine tr	364	59	4.7	43	4	AAAF54328	Aaf54328 Probe #28
292	61	4.8	207	6	ABV88239	Abv88239 Human col	365	59	4.7	43	8	ACD68365	AcD68365 Novel hum
293	61	4.8	228	2	AAAT33746	Aat33746 Cellubrev	366	59	4.7	43	8	ACH04467	Ach04467 Human sec
294	61	4.8	228	3	AAA39892	Aaa39892 Human cel	367	59	4.7	43	8	ACD68011	AcD68011 Novel hum
295	61	4.8	228	9	AD60722	Ad60722 Human lun	368	59	4.7	43	9	ADC18047	AdC18047 Human PRO
296	60.5	4.8	150	2	AAQ04061	Aaq04061 Homologou	369	59	4.7	43	9	ADD70693	AdD70693 Human sec
C 297	60.5	4.8	196	9	ADD49332	Add49332 Human lun	370	59	4.7	43	9	ADD39770	AdD39770 Human sec
C 298	60.5	4.8	222	6	ABL85865	AbL85865 Human ova	371	59	4.7	43	9	ADD70216	AdD70216 Human sec
C 299	60	4.8	51	4	AAI33111	Aai33111 Human SNP	372	59	4.7	43	9	ADD38337	AdD38337 Human sec
300	60	4.8	64	6	ABQ78134	Abq78134 Synthetic	373	59	4.7	43	9	ADD39293	AdD39293 Human sec

374	59	4.7	43	9	ADD38816	Human sec	C 447	56	4.5	173	4	AAK48795	Human bon
375	59	4.7	43	9	ADD40247	Human sec	C 448	56	4.5	173	4	AAK22627	Human bra
376	59	4.7	43	9	ADE50468	Human sec	C 449	56	4.5	173	4	ABS48468	Human liv
377	59	4.7	43	9	ADE20080	Human sec	C 450	56	4.5	173	6	ABS22500	Human gen
378	59	4.7	43	9	ADE49991	Human sec	C 451	56	4.5	200	6	RAA41230	Targeting
379	59	4.7	43	9	ADE21549	Human sec	C 452	55.5	4.4	65	2	AAK78016	Chimeric
380	59	4.7	60	2	AAT89213	Prostrate	C 453	55.5	4.4	125	2	AAQ49771	CAP37 pro
381	59	4.7	65	6	ABN53152	Mouse spl	C 454	55.5	4.4	159	4	AAI20273	Probe #10
382	59	4.7	84	2	AAQ3781	Bovine tr	C 455	55.5	4.4	139	4	ABA65308	Human foe
383	59	4.7	84	2	AAQ3780	Bovine tr	C 456	55.5	4.4	159	4	AAI48343	Probe #17
384	59	4.7	192	4	AAAS58355	CDNA #103	C 457	55.5	4.4	159	4	AAI45475	Probe #14
385	59	4.7	192	4	AAAS58005	CDNA #681	C 458	55.5	4.4	159	4	ABA47420	Human bra
386	59	4.7	192	4	ABK45393	CDNA #935	C 459	55.5	4.4	159	4	ABA32409	Probe #10
387	59	4.7	196	4	AAAS58259	Human ova	C 460	55.5	4.4	159	4	AAK39463	Human bon
388	59	4.7	220	5	AAH82644	Human sec	C 461	55.5	4.4	159	4	AAK13721	Human bra
389	58.5	4.7	119	3	AAAC21698	Human sec	C 462	55.5	4.4	159	4	ABS39053	Human liv
390	58.5	4.7	173	2	AAQ06661	Synthetic	C 463	55.5	4.4	159	5	AAI05977	Probe #59
391	58.5	4.7	184	2	AAQ06658	Synthetic	C 464	55.5	4.4	159	6	ABS13552	Human gen
392	58	4.6	213	2	AAT39203	Aspergill	C 465	55.5	4.4	173	3	AAO5467	Human sec
393	58	4.6	213	2	AAO5393	Aspergill	C 466	55.5	4.4	199	4	AAI26596	Probe #16
394	58	4.6	219	2	AAK88514	Conus tex	C 467	55.5	4.4	199	4	ABA74831	Human foe
395	58	4.6	219	2	AAT34867	Plasmid p	C 468	55.5	4.4	199	4	AAI5357	Probe #24
396	58	4.6	225	2	AAKX0683	Human sec	C 469	55.5	4.4	199	4	ABA39530	Probe #17
397	57.5	4.6	201	2	AAQ61184	Human bra	C 470	55.5	4.4	199	4	AAK49483	Human bon
398	57.5	4.6	228	5	AAAT7528	DNA encod	C 471	55.5	4.4	199	4	AAK23326	Human bra
399	57.5	4.6	229	2	AAQ06485	Intestina	C 472	55.5	4.4	199	4	ABS49104	Human liv
400	57.5	4.6	229	2	AAQ12219	SMUC-42 i	C 473	55.5	4.4	199	6	ABS32967	Human gen
401	57	4.5	39	2	AAV72615	Rat Facto	C 474	55.5	4.4	207	2	AAI49125	Partial D
402	57	4.5	39	2	AAZ09551	Rat Facto	C 475	55.5	4.4	207	7	ABX48051	Bovine ES
403	57	4.5	59	6	ABQ78143	Synthetic	C 476	55.5	4.4	210	3	AAK75138	Human ORF
404	57	4.5	60	6	ABN36010	Human spl	C 477	55.5	4.4	210	6	ABN26622	Human ORF
405	57	4.5	65	6	ABN28536	Rat splic	C 478	55.5	4.4	221	6	ABL74879	Corn tass
406	57	4.5	163	5	ABV37921	Human pro	C 479	55.5	4.4	222	6	ABK79202	Bacillus
407	57	4.5	186	4	AAK31229	Human dig	C 480	55	4.4	51	4	AAH93885	P703P epi
408	57	4.5	186	4	AAK91228	Human dig	C 481	55	4.4	51	4	AAK64121	Human pro
409	57	4.5	189	6	ABK38988	CDNA encd	C 482	55	4.4	51	5	ACA59929	Prostate
410	57	4.5	189	7	ACA11317	Human lun	C 483	55	4.4	51	6	ABL55492	Prostate
411	57	4.5	189	7	ACA02503	Long carc	C 484	55	4.4	51	7	ACC95656	Prostate
412	57	4.5	192	4	AAI26092	Probe #16	C 485	55	4.4	51	9	ADB14243	Human pro
413	57	4.5	192	4	ABAT73369	Human foe	C 486	55	4.4	192	4	AAI01619	Human rep
414	57	4.5	192	4	AAI53801	Probe #22	C 487	55	4.4	192	6	ABK45188	cDNA enco
415	57	4.5	192	4	ABA38723	Probe #17	C 488	55	4.4	195	7	ABX40740	Bovine ES
416	57	4.5	192	4	AAK47972	Human bon	C 489	55	4.4	198	4	ABL27031	Drosophil
417	57	4.5	192	4	AAK21809	Human bra	C 490	55	4.4	219	5	AAK60212	Synthetic
418	57	4.5	192	4	ABS47687	Human liv	C 491	55	4.4	222	6	ABS23868	Human gen
419	57	4.5	192	6	ABS21925	Human gen	C 492	55	4.4	225	6	ABN76329	Human ORF
420	57	4.5	196	2	AAQ06670	Synthetic	C 493	55	4.4	226	7	ACC41378	Perennial
421	57	4.5	200	7	ABS56432	3' mouse	C 494	55	4.4	228	9	ADC92223	E. faeciu
422	57	4.5	204	3	AAO08706	Human sec	C 495	54.5	4.3	132	3	AAO4559	Human sec
423	57	4.5	208	2	AAQ50639	Sequence	C 496	54.5	4.3	132	3	AAO4559	Human sec
424	57	4.5	213	2	AAT39199	Aspergill	C 497	54.5	4.3	212	3	AAK38167	Human sec
425	57	4.5	213	2	AAO5389	Aspergill	C 498	54	4.3	30	6	AAK20771	Mutagenic
426	57	4.5	214	5	ABV37490	Human pro	C 499	54	4.3	30	6	AAK20771	Mutagenic
427	57	4.5	215	2	AAK37691	Human EST	C 500	54	4.3	60	6	ABN34991	Human spl
428	57	4.5	219	6	ABX04842	Conus sp							
429	57	4.5	219	6	ABX04841	Conus sp							
430	57	4.5	221	6	ABS1604	Human cDN							
431	56.5	4.5	142	4	ABA66673	Human foe							
432	56.5	4.5	142	4	ABA48764	Human bre							
433	56.5	4.5	142	4	AAK40832	Human bon							
434	56.5	4.5	142	5	AAI07295	Probe #72							
435	56.5	4.5	177	6	ABN25452	Human ORF							
436	56.5	4.5	215	5	ABV33602	Human pro							
437	56.5	4.5	216	4	AAK55246	Human imm							
438	56	4.5	50	4	AAAD03663	Human ser							
439	56	4.5	64	2	AAK78015	Chimeric							
440	56	4.5	65	6	ABN28546	Rat splic							
441	56	4.5	146	4	ABA66775	Human foe							
442	56	4.5	146	6	ABK14886	Human gen							
443	56	4.5	159	6	ABV98601	Human pan							
444	56	4.5	160	5	ABA06312	Soy bean							
445	56	4.5	173	4	ABA74172	Human foe							
446	56	4.5	173	4	AAI54624	Probe #23							

ALIGNMENTS

RESULT 1
 ABK48915
 ID ABK48915 standard; DNA; 153 BP.

AC ABK48915;

DT 02-JUL-2002 (first entry)

XX Novel human kallikrein KLK15, intron 5.

XX Kallikrein; KLK15; cancer; prostate cancer; kidney cancer;
 testicular cancer; thyroid disorder; chromosome 19q13.3-q13.4; ds.

XX Homo sapiens.

PN WO200214485-A2.
 XX
 PD 21-FEB-2002.
 XX
 PF 10-AUG-2001; 2001WO-CA001141.
 XX
 PR 11-AUG-2000; 2000US-0224853P.
 XX
 PA (MOUN) MOUNT SINAI HOSPITAL.
 XX
 PI Yousef GM, Diamandis BP;
 XX
 PI WPI; 2002-329575/36.
 XX
 DR Novel kallikrein protein, KLK15 and nucleic acid molecule encoding the
 PT protein useful for diagnosing, monitoring and treating thyroid disorders
 PT and cancer, particularly prostate, colon, kidney and testicular cancer.
 XX
 PS Claim 3; Page 63; 67pp; English.
 XX
 CC The invention describes an isolated kallikrein protein (I) (KLK15) and
 CC splice variants of (I). (I) is useful for identifying a substance which
 CC associates with (I) and for evaluating a compound for its ability to
 CC modulate the biological activity of (I). An anti-(I) antibody labelled
 CC with a detectable substance is useful to detect KLK15 polypeptide in
 CC biological samples, tissues and cells. The antibody is also useful for
 CC monitoring the progression of cancer in an individual. (I) and the
 CC polynucleotide encoding it are useful for treatment of a condition
 CC mediated by KLK15 protein, in particular cancer (including prostate,
 CC colon, kidney and testicular cancer) and thyroid disorders. This sequence
 CC (located on chromosome 19q13.3-q13.4) represents intron 5 of the gene
 CC encoding the novel human kallikrein protein (see ABK48346) described in
 CC the invention
 XX
 SQ Sequence 153 BP; 33 A; 38 C; 49 G; 33 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: Length: 153
 Score: 206.00 Matches: 36
 Percent Similarity: 80.00% Conservative: 4
 Best Local Similarity: 72.00% Mismatches: 10
 Query Match: 16.38% Indels: 0
 DB: 6 Gaps: 0
 US-09-856-320A-2_COPY_54_282 (1-229) x ABK48915 (1-153)
 QY 180 GlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGly 199
 Db 1 GGTGACTCTGGGGACCCCTGCTGTGGGGGCATCTTCGAGGCGATTGTCTCTGGGGT 60
 QY 200 GlnAspProCysAlaIleThrArgLysProGlyValThrThrLysValCysLysTyrVal 219
 Db 61 GACGTCCCTTGTGACACACACCAAGCCCTGGTGTCTATACCAAAAGTCTGCCACTACTTG 120
 QY 220 AspTrpIleGlnGluThrMetLysAsnAn 229
 Db 121 GAGTGGATCAGGGAACCATGAAGAGGAAC 150
 RESULT 2
 ID AAS24516
 ID AAS24516 standard; cDNA; 205 BP.
 XX
 AC AAS24516;
 XX
 DT 07-NOV-2001 (first entry)
 XX
 DE Human ovarian PCR-subtracted cDNA library clone #697.
 XX
 KW Immunogenic protein; cancer; ovarian tumour; T-cell stimulation; ss;
 KW gene therapy; cytostatic; T-cell expansion; nucleic acid hybridisation;
 KW primer; probe.
 XX
 OS Homo sapiens.

XX WO200157207-A2.
 PN
 XX
 PD 09-AUG-2001.
 XX
 PF 05-FEB-2001; 2001WO-US003733.
 XX
 PR 04-FEB-2000; 2000US-0180403P.
 XX
 PR 28-MAR-2000; 2000US-0192745P.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Algate PA, Mannion J;
 XX
 PI WPI; 2001-488879/53.
 XX
 DR New polynucleotides encoding ovarian tumor proteins, useful for treating
 PT ovarian cancer, and as probes, primers, and markers of cancer
 PT progression.
 XX
 PS Example 1; Page 225; 378pp; English.
 XX
 CC The invention comprises compositions used for the therapy and diagnosis
 CC of ovarian cancer. The compositions comprise one or more ovarian tumour
 CC proteins, their associated polynucleotides, or immunogenic portions of
 CC the proteins. The ovarian tumour polynucleotides and polypeptides are
 CC useful for stimulating and/or expanding T cells specific for a tumour
 CC protein. They are also useful for inhibiting the development of cancer in
 CC a patient with an ovarian tumour DNA or protein by incubating isolated T-
 CC cells allowing them to proliferate, and administering to the patient. The
 CC sequences can be used as markers for cancer, for example, to monitor
 CC ovarian cancer progression. Probes and primers are useful in nucleic acid
 CC hybridisation, in detecting the presence of complementary sequences in a
 CC given sample, for preparing mutant species and for preparing other
 CC genetic constructions. Sequences AAS23820-AAS25231 and AAS25238-AAS25549
 CC represent human ovarian tumour protein cDNA clones
 XX
 SQ Sequence 205 BP; 38 A; 67 C; 56 G; 44 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: Length: 205
 Score: 202.50 Matches: 34
 Percent Similarity: 73.53% Conservative: 16
 Best Local Similarity: 50.00% Mismatches: 17
 Query Match: 16.10% Indels: 1
 DB: 4 Gaps: 1
 US-09-856-320A-2_COPY_54_282 (1-229) x AAS24516 (1-205)
 QY 142 CysAlaAsnIleThrIleIleGluHisGlnLysCysGluAsnAlaTyrProGlyAsnIle 161
 Db 4 TGTCTCCAGCATCTACTCTCTGAGCCCTAAGAGTGTGAGGTCTTCTACCTGGCGTGGTC 63
 QY 162 ThrAspThrMetValCysAlaSerValGlnGlyGlyLysAspSerCysGlnGlyAsp 181
 Db 64 ACCAACCAACATGATGTGTGGACTG---GACCGGGGCCAGGACCCCTTCCAGAGTGAC 120
 QY 182 SerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGlnAsp 201
 Db 121 TCTGGAGGCCCCCTGGCCTGTGAGGAGACCCCTCCAGGCATCTCTCTCGTGGGTGTTTAC 180
 QY 202 ProCysAlaIleThrArgLysPro 209
 Db 181 CCTGTGGCTCTGCCAGCATCCA 204
 RESULT 3
 ID ADA05697
 ID ADA05697 standard; cDNA; 178 BP.
 XX
 AC ADA05697;
 XX
 DT 06-NOV-2003 (first entry)
 XX

Human NOV1lf encoding cDNA SEQ ID NO:57.

XX human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
 KW immunomodulator; cytostatic; nootropic; neuroprotective;
 KW antiparkinsonian; antilipase; gene therapy; human disease;
 KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
 KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
 KW immune disorder; haematopoietic disorder; dyslipidaemia; gene; ss.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FT CDS 2..1178
 FT /*tag= a
 FT /product= "NOV1lf"
 XX WO2003029424-A2.
 XX 10-APR-2003.
 XX 02-OCT-2002; 2002WO-US031373.
 XX 02-OCT-2001; 2001US-0326483P.
 XX 05-OCT-2001; 2001US-0327435P.
 XX 05-OCT-2001; 2001US-0327449P.
 XX 09-OCT-2001; 2001US-0327917P.
 XX 09-OCT-2001; 2001US-0328029P.
 XX 03-OCT-2001; 2001US-0328044P.
 XX 09-OCT-2001; 2001US-0328056P.
 XX 12-OCT-2001; 2001US-0328849P.
 XX 15-OCT-2001; 2001US-0329414P.
 XX 17-OCT-2001; 2001US-0330142P.
 XX 18-OCT-2001; 2001US-0330309P.
 XX 22-OCT-2001; 2001US-0341058P.
 XX 24-OCT-2001; 2001US-0339266P.
 XX 24-OCT-2001; 2001US-0343629P.
 XX 29-OCT-2001; 2001US-0349575P.
 XX 01-NOV-2001; 2001US-0346357P.
 XX 17-APR-2002; 2002US-0373260P.
 XX 19-APR-2002; 2002US-0373815P.
 XX 19-APR-2002; 2002US-0373817P.
 XX 13-APR-2002; 2002US-0373826P.
 XX 19-APR-2002; 2002US-0373884P.
 XX 22-APR-2002; 2002US-0374977P.
 XX 16-MAY-2002; 2002US-0381037P.
 XX 16-MAY-2002; 2002US-0381038P.
 XX 17-MAY-2002; 2002US-0381042P.
 XX 28-MAY-2002; 2002US-0381642P.
 XX 29-MAY-2002; 2002US-0383656P.
 XX 25-JUN-2002; 2002US-0383831P.
 XX 01-OCT-2002; 2002US-0391335P.
 XX 01-OCT-2002; 2002US-00262511.
 XX (CURA-) CURAGEN CORP.
 XX Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
 PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Nalvankar UM;
 PI Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
 PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Shenoy SG;
 PI Shimkets RA, Rothenberg ME, Leach VD, Agee ML, Berghs C, Dipippo VA;
 PI Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
 XX WPI: 2003-381626/36.
 DR P-PSDB; ADA05698.
 XX New NOVX polypeptides and nucleic acids, useful for diagnosing,
 PT preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,
 PT cancer or dyslipidaemia, and in chromosome mapping, tissue typing or
 PT pharmacogenomics.
 XX Claim 20; Page 143; 586pp; English.
 PS The present invention describes NOVX proteins, where X can be 1 to 55
 XX

CC (e.g. NOV1). Also described: (1) a composition comprising a polypeptide
 CC described above and a carrier; (2) a kit comprising, in one or more
 CC containers, the composition described above; (3) an isolated nucleic acid
 CC molecule which encodes a NOVX protein of the invention; (4) a vector
 CC comprising the nucleic acid molecule described above; (5) a cell
 CC comprising the above vector; (6) an antibody that immunospecifically
 CC binds to the polypeptide described above; (7) methods for determining the
 CC presence or amount of the above polypeptide or nucleic acid molecule in a
 CC sample; (8) methods for determining the presence of or predisposition to
 CC a disease associated with altered levels of expression of the above
 CC polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
 CC method of identifying an agent that binds to the polypeptide described
 CC above; (10) a method for identifying a potential therapeutic agent for
 CC use in treating a pathology that is related to an aberrant expression or
 CC aberrant physiological interactions of the polypeptide; (11) a method of
 CC screening for a modulator of activity or of latency or predisposition to
 CC a pathology associated with the polypeptide; (12) a method for modulating
 CC the activity of the polypeptide described above; (13) methods of treating
 CC or preventing a pathology associated with the above polypeptide in a
 CC mammal; and (14) a method for producing the above polypeptide. NOVX
 CC sequences have antidiabetic, anorectic, antibacterial, virucide,
 CC immunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian
 CC and antilipase activities, and can be used in gene therapy. The
 CC polypeptide is useful in manufacturing a medicament for treating a
 CC syndrome associated with a human disease. The polypeptide or the nucleic
 CC acid molecule may be used to diagnose, treat or prevent metabolic
 CC disorders such as diabetes or obesity, infections, cachexia, cancer,
 CC neurodegenerative disorders such as Alzheimer's disease or Parkinson's
 CC disease, immune disorders, haematopoietic disorders and various
 CC dyslipidaemias. The nucleic acids can also be used as hybridisation
 CC probes, in chromosome mapping, tissue typing, preventive medicine and
 CC pharmacogenomics. The present sequence encodes a human NOVX protein from
 CC the present invention.

SQ Sequence 178 BP; 37 A; 53 C; 57 G; 31 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 4,7e-09 Length: 178
 Score: 194.00 Matches: 32
 Percent Similarity: 83.33% Conservative: 8
 Best Local Similarity: 66.67% Mismatches: 8
 Query Match: 15.42% Indels: 0
 DB: 7 Gaps: 0

US-09-856-320A-2_COPY_54_282 (1-229) x ADA05697 (1-178)

Qy 177 SerCysGlnGlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIle 196
 Db 8 TCCGGGCAGGGCGATTCTGGAGGCCCTCTGGTGTGATGGTCACTCCAGGGCATCACA 67
 Qy 197 SerTrpGlnAspProCysAlaIleThrArgLysProGlyValThrLysValCys 216
 Db 68 TCTGGGGCTCAGACCCCTGTGGAGGTCGACAAACCTGGCGCTATACCAACATCTGC 127
 Qy 217 LysTrpValAspTrpIleGlnGlu 224
 Db 128 CGGTACTCGGACTGGATCAAGAAG 151

RESULT 4

AAZ95014
 ID AAZ95014 standard; cDNA; 198 BP.

XX AC AAZ95014;

XX AC AAZ95014;

XX 15-AUG-2000 (first entry)

XX Prostate cancer specific gene clone 2626135H1.

XX Prostate cancer; cancer specific gene; CSG; diagnosis; monitoring;
 KW staging; imaging; therapy; metastasis; marker; human; ss.
 XX OS Homo sapiens.

PN WO200023111-AL.

XX

PD 27-APR-2000.

XX

PF 19-OCT-1999; 99WO-US024331.

XX

PR 19-OCT-1998; 98US-0104737P.

XX

PA (DIAD-) DIADEXUS LLC.

XX

PI Salceda S, Recipon H, Caferkey R;

XX

PP WFI; 2000-339531/29.

XX

PT Diagnosing, staging and monitoring the presence and metastases of

PT prostate cancer especially useful for treating prostate cancer comprises

PT measuring changes in cancer specific gene levels.

XX

PS Claim 7; Page 65; 74pp; English.

XX

CC The present sequence is that of cancer specific gene (CSG) clone

CC 262613SH1, which was identified in a database search using the data

CC mining Cancer Leads Automatic Search Package (CLASP), which allows the

CC identification of highly expressed organ and cancer specific genes. The

CC invention provides ESTs and full-length contigs for prostate CSs (see

CC AAZ9498-495017). The CSGs, polypeptides encoded by them, and antibodies

CC that specifically bind CSG are used in new, claimed methods for

CC detecting, diagnosing, monitoring, staging, imaging and treating prostate

CC cancer. The new methods provide earlier diagnosis for the presence and

CC metastasis of prostate cancer, and can be used to determine if a cancer

CC has metastasized, or to monitor the progress or stage of the disease when

CC it has not metastasized

XX

SQ Sequence 198 BP; 39 A; 58 C; 60 G; 40 T; 0 U; 1 Other;

Alignment Scores:

Pred. No.: 1.87e-05 Length: 198

Score: 188.00 Matches: 31

Percent Similarity: 70.69% Conservative: 10

Best Local Similarity: 53.45% Mismatches: 17

Query Match: 14.94% Indels: 0

DB: 3 Gaps: 0

US-09-856-320A-2_COPY_54_282 (1-229) x AAZ95014 (1-198)

QY 164 ThrMetValCysAlaSerValGlnGluglyGlyLysAspSerCysGlnGlyAspSerGly 183

Db 17 AGCATGTTCCTCGCGCGGGAGGACAGACAGAGGACTCTCTGCACCGTGACTCTGG 76

QY 184 GlyProLeuValCysAsnGlnSerLeuGlnGlylleleSerrTrpGlyGlnaspProcys 203

Db 77 GGSCCCCCATGATCTGCAACGGGTACTTTCAGGGCCTGTGTCTTCGAAAAGCCCGGT 136

QY 204 AlaIleThrArgLysProGlyValTyThrLysValCysLysTyrrValAspTrp 221

Db 137 GGCCAAAGTTGGCGTCCAGGTTGTCTACACCAACTCTGCAAAATTCATGAGTG 190

RESULT 5

ABN17410

ID ABN17410 standard; cDNA; 220 BP.

XX

AC ABN17410;

XX

DT 24-JUN-2002 (first entry)

XX

DE Human OREFX polynucleotide sequence SEQ ID NO:3297.

XX

KW Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;

KW hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;

KW degenerative disorder; osteoarthritis; neurodegenerative disorder;

KW cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;

KW hypertension; hypothyroidism; cholesterol ester storage disease;

KW immune deficiency; immune disorder; infectious disease;

Db 165 GGTGTAAGACATCTGGGGGGGATCTGGGGGTCACCTGCTGTGAATGGTGGCTT 106
Qy 193 GlnGlyIleIleSerTrpGlyGlnAspProCysAlaIleThrArgLysProGlyValTyr 212
Db 105 CAAGGTATCACATCATGCGGCGCTGAGCCATGTGCCCTGCTGAAAGCCCTGCTGTGTAC 46

RESULT 8
AAV60379
ID AAV60379 standard; mRNA; 200 BP.
XX
AC AAV60379;
XX
DT 07-DEC-1998 (first entry)
XX
DE mRNA target sequence from exons 2 and 3 of PSA gene.
XX
KW mRNA target sequence; prostate specific antigen; PSA; RNA purification;
XX ds.
OS Homo sapiens.
XX
PN US5817798-A.
XX
PD 06-OCT-1998.
XX
PF 17-SEP-1997; 97US-00931981.
XX
PR 17-SEP-1997; 97US-00931981.
XX
PA (ABBO) ABBOTT LAB.
XX
PI Gundling GJ;
XX
XQ WPI; 1998-556473/47.
XX
XX Purification of RNA, used for nucleic acid amplification and disease
XX detection - by precipitating other sample components with transition
XX metal ions, separating and collecting the purified RNA.
XX
XX Example 5; Col 9-10; 6pp; English.
XX
XX The present sequence represents a mRNA target sequence from exons 2 and 3
XX of the prostate specific antigen (PSA) gene. The sequence is used to
XX exemplify the invention. The specification describes a method for
XX purifying RNA. The method comprises contacting a test sample with
XX polyvalent transition metal ions to form a precipitant and a supernatant,
XX separating the precipitant from the supernatant, and collecting the
XX supernatant to obtain a purified solution of total RNA. The RNA is used
XX for nucleic acid amplification and disease detection
XX
XQ Sequence 200 BP; 31 A; 58 C; 67 G; 44 T; 0 U; 0 Other;

Db 156 CACTGCATCAGGAACAAAGCGTGATCTTGTGGTGGGCACAGC 200
RESULT 9
ABK48905
ID ABK48905 standard; DNA; 154 BP.
XX
AC ABK48905;
XX
DT 02-JUL-2002 (first entry)
XX
DE Novel human kallikrein KLK15, exon 2.
XX
KW Kallikrein; KLK15; cancer; prostate cancer; colon cancer; kidney cancer;
XX testicular cancer; thyroid disorder; chromosome 19q13.3-q13.4; ds.
XX
OS Homo sapiens.
XX
PN WO200214485-A2.
XX
PD 21-FEB-2002.
XX
PF 10-AUG-2001; 2001WO-CA001141.
XX
PR 11-AUG-2000; 2000US-0224953P.
XX
PA (MOUN) MOUNT SINAI HOSPITAL.
XX
XX Yousef GM, Diamandis EP;
XX
XX WPI; 2002-329575/36.
XX
XX Novel kallikrein protein, KLK15 and nucleic acid molecule encoding the
XX protein useful for diagnosing, monitoring and treating thyroid disorders
XX and cancer, particularly prostate, colon, kidney and testicular cancer.
XX
XX Claim 3; Page 61; 67pp; English.
XX
XX The invention describes an isolated kallikrein protein (I) (KLK15) and
XX splice variants of (I). (I) is useful for identifying a substance which
XX associates with (I) and for evaluating a compound for its ability to
XX modulate the biological activity of (I). An anti-(I) antibody labelled
XX with a detectable substance is useful to detect KLK15 polypeptide in
XX biological samples, tissues and cells. The antibody is also useful for
XX monitoring the progression of cancer in an individual. (I) and the
XX polynucleotide encoding it are useful for treatment of a condition
XX mediated by KLK15 protein, in particular cancer (including prostate,
XX colon, kidney and testicular cancer) and thyroid disorders. This sequence
XX (located on chromosome 19q13.3-q13.4) represents exon 2 of the gene
XX encoding the novel human kallikrein protein (see ABK48346) described in
XX the invention
XX
XQ Sequence 154 BP; 28 A; 51 C; 44 G; 31 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.98e-06 Length: 154
Score: 164.00 Matches: 26
Percent Similarity: 83.33% Conservative: 9
Best Local Similarity: 61.30% Mismatches: 7
Query Match: 13.04% Indels: 0
DB: 6 Gaps: 0
US-09-856-320A-2_COPY_54_282 (1-229) x ABK48905 (1-154)
Qy 1 IleIleLysGlyPheGluCysLysProHisSerGlnProTrpGlnAlaLeuPheGlu 20
Db 21 TTGCTGGAGAGGTGACAGAGTGTGCACCCCATCTCCAGCCATGGCAGTGGCTCTCTACGAG 80
Qy 21 LysThrArgLeuLeuCysGlyAlaThrLeuLeuAlaProArgTrpLeuLeuThrAlaAla 40
Db 81 CGTGGACGCGTTTAACTGTGGGGCTTCCTCTCATCTCCACACATGGGTCTGTCTGGGCC 140
Qy 41 HisCys 42

Db 165 GGTGTAAGACATCTGGGGGGGATCTGGGGGTCACCTGCTGTGAATGGTGGCTT 106
Qy 193 GlnGlyIleIleSerTrpGlyGlnAspProCysAlaIleThrArgLysProGlyValTyr 212
Db 105 CAAGGTATCACATCATGCGGCGCTGAGCCATGTGCCCTGCTGAAAGCCCTGCTGTGTAC 46
RESULT 8
AAV60379
ID AAV60379 standard; mRNA; 200 BP.
XX
AC AAV60379;
XX
DT 07-DEC-1998 (first entry)
XX
DE mRNA target sequence from exons 2 and 3 of PSA gene.
XX
KW mRNA target sequence; prostate specific antigen; PSA; RNA purification;
XX ds.
OS Homo sapiens.
XX
PN US5817798-A.
XX
PD 06-OCT-1998.
XX
PF 17-SEP-1997; 97US-00931981.
XX
PR 17-SEP-1997; 97US-00931981.
XX
PA (ABBO) ABBOTT LAB.
XX
PI Gundling GJ;
XX
XQ WPI; 1998-556473/47.
XX
XX Purification of RNA, used for nucleic acid amplification and disease
XX detection - by precipitating other sample components with transition
XX metal ions, separating and collecting the purified RNA.
XX
XX Example 5; Col 9-10; 6pp; English.
XX
XX The present sequence represents a mRNA target sequence from exons 2 and 3
XX of the prostate specific antigen (PSA) gene. The sequence is used to
XX exemplify the invention. The specification describes a method for
XX purifying RNA. The method comprises contacting a test sample with
XX polyvalent transition metal ions to form a precipitant and a supernatant,
XX separating the precipitant from the supernatant, and collecting the
XX supernatant to obtain a purified solution of total RNA. The RNA is used
XX for nucleic acid amplification and disease detection
XX
XQ Sequence 200 BP; 31 A; 58 C; 67 G; 44 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 1.2e-06 Length: 200
Score: 168.00 Matches: 25
Percent Similarity: 74.55% Conservative: 16
Best Local Similarity: 45.45% Mismatches: 14
Query Match: 13.35% Indels: 0
DB: 2 Gaps: 0
US-09-856-320A-2_COPY_54_282 (1-229) x AAV60379 (1-200)
Qy 1 IleIleLysGlyPheGluCysLysProHisSerGlnProTrpGlnAlaLeuPheGlu 20
Db 36 ATTGTGGAGGCTGGGAGTGGAGAGCAATCCCAACCTGGCAGGTGCTTTGTGGGCTCT 95
Qy 21 LysThrArgLeuLeuCysGlyAlaThrLeuLeuAlaProArgTrpLeuLeuThrAlaAla 40
Db 96 CGTGGACGCGAGTCTGCGGGGGTGTCTGTGTGACCCCGGTCCTCACAGTGGCC 155
Qy 41 HisCysLeuLysProArgTyrIleValHisLeuGlyGlnHisAsn 55

DB: 6 Gaps: 1

US-09-856-320A-2_COPY_54_282 (1-229) x ABN89908 (1-202)

Qy 183 GlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleSerTrpGlyGlnAspPro 202
 Db 2 GGTAGCACTGTGGTCTGCAATAGAGAACTCCAGGGTATAGTCTCTCTGGGGCTATGGC--- 58
 Qy 203 CysAlaIleThrArgLysProGlyValThrLysValCysLysTyrValAspTrpIle 222
 Db 59 TGTGCGCTGCCAGCAAACTCCCTGGTGTGTACACCAAGGTCTGCAACTATGTGGACTGGATT 118
 Qy 223 GlnGluThrMetLysAsnAsn 229
 Db 119 CAGGACACAATGTGCCCAAC 139

RESULT 12
 ID AAT40842
 AC AAT40842;
 DT 15-MAR-1997 (first entry)
 XX Serine protease nFSP12 C-terminal fragment gene.
 DE
 XX
 XX Flea; midgut; serine protease; nFSP12; recombinant vaccine;
 KW domestic animal; infestation; insecticide; protease-inhibitor;
 KW controlled release formulation; synergist; ss.
 XX
 OS Siphonaptera sp.
 XX
 XX WO9611706-A1.
 XX
 XX
 PD 25-APR-1996.
 XX
 XX 18-OCT-1995; 95WO-US014442.
 XX
 XX 18-OCT-1994; 94US-00326773.
 PR 07-JUN-1995; 95US-00482130.
 PR 07-JUN-1995; 95US-00484211.
 PR 07-JUN-1995; 95US-00485443.
 PR 07-JUN-1995; 95US-00485455.
 XX
 XX (HESK-) HESKA CORP.
 XX
 XX Grieve RB, Rushlow KE, Hunter SW, Frank GR, Stiegler GL, Heath A;
 PI Yamanaka M, Arfsten A, Dale B;
 PI
 XX WPI; 1996-221762/22.
 DR P-PSDB; AAM01197.
 XX
 XX DNA encoding Flea serine protease and aminopeptidase - useful in vaccines
 PT to protect animals from flea infestation.
 XX
 XX Claim 70; Page 169; 241pp; English.
 XX
 CC This sequence encodes a C-terminal fragment of a flea midgut serine
 CC protease, nFSP12-225 (AAT40854), and has been isolated from a flea cDNA
 CC library by PCR using primers AAT40862-63 and hybridisation with probe
 CC AAT40866, based on conserved serine protease sequences. A corresponding N
 CC-terminal fragment, nFSP12-144 (AAT40836). The sequence may be used to
 CC produce a recombinant vaccine for protection of domestic animals from
 CC flea infestation, or in isolation of protease-inhibitors which may be
 CC used in controlled release formulations to reduce the flea burden on and
 CC around the animal. The inhibitors may be included in insecticidal
 CC compositions to increase efficacy of other active compounds, by reducing
 CC proteolytic activity in the flea midgut
 XX
 SQ Sequence 207 BP; 55 A; 41 C; 47 G; 64 T; 0 U; 0 Other;
 Alignment Scores: 5.29e-05 Length: 207
 Pred. No.:

Score: 150.00 Matches: 32
 Percent Similarity: 72.73% Conservative: 8
 Best Local Similarity: 58.18% Mismatches: 13
 Query Match: 11.92% Indels: 3
 DB: 2 Gaps: 2

US-09-856-320A-2_COPY_54_282 (1-229) x AAT40842 (1-207)

Qy 175 LysAspSerCysGlnGlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGly 194
 Db 43 AAGGTGCATGTAAAGGTGATTCGGTGGCCCTTACTCATCATGACAACTTCATGGA 102
 Qy 195 IleIleSerTrpGlyGlnAspProCysAlaIleThrArgLysProGlyValThrLys 214
 Db 103 ATTGTTCTCTGGGGC---ATTCTTGGCTGT---CGCAAGCCTGATGTATTCAAGA 155
 Qy 215 ValCysLysTyrValAspTrpIleGlnGluThrMetLysAsnAsn 229
 Db 156 GTTCTCATTTATGTCGATTGGATTAAATCCAAATTTGAATAAAT 200

RESULT 13
 AAC90850
 ID AAC90850 standard; cDNA; 207 BP.
 XX
 AC AAC90850;
 XX
 DT 19-MAR-2001 (first entry)
 XX
 DE Flea serine protease nFSP12 N-terminal nucleotide sequence #76.
 XX
 KW Flea; cat flea; serine protease; aminopeptidase; cysteine protease;
 KW flea infestation; proteolytic; insecticide; vaccine; cat; dog; flea;
 KW Ctenocephalides felis; Ctenocephalides canis; Pulex irritans;
 KW ectoparasite; ss.
 XX
 OS Ctenocephalides felis.
 XX
 XX US6150125-A.
 XX
 PD 21-NOV-2000.
 XX
 PF 24-APR-1996; 96US-00639075.
 XX
 PR 13-DEC-1991; 91US-00806482.
 PR 18-OCT-1994; 94US-00326773.
 PR 07-JUN-1995; 95US-00482130.
 PR 07-JUN-1995; 95US-00484211.
 PR 07-JUN-1995; 95US-00485443.
 PR 07-JUN-1995; 95US-00485455.
 PR 15-AUG-1997; 97WO-US014442.
 XX
 XX (HESK-) HESKA CORP.
 XX
 XX Gaines PJ, Silver G, Rushlow KE, Hunter SW, Frank GR;
 PI Stiegler GL, Grieve RB;
 PI
 XX WPI; 2001-136374/14.
 DR P-PSDB; AAB50594.
 XX
 PT New isolated flea proteins with proteolytic activity, useful for
 PT preventing and reducing flea infestations in mammals especially cats and
 PT dogs.
 XX
 PS Claim 4; Col 51-52; 150pp; English.
 XX
 CC The present invention describes isolated flea serine protease,
 CC aminopeptidase and cysteine protease proteins (I). Also described is a
 CC method for identifying a compound (II) capable of inhibiting flea
 CC protease activity comprising: (a) contacting (I) with a protease
 CC substrate and a putative inhibitory compound, where (I) has proteolytic
 CC activity in the absence of the compound; and (b) determining if the
 CC compound inhibits protease activity by detecting cleavage of the protease
 CC substrates; where decreased cleavage of the protease substrate indicates

XX 16-APR-1996; 96US-0015765P.
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 XX Robbins DJ;
 XX WPI; 1997-526473/48.
 XX Monitoring or diagnosis of prostate cancer - by detecting prostate-
 PT specific antigen mRNA using specific primers.
 XX Disclosure; Page 16; 25pp; English.
 XX cDNA sequences AAT92974-77 encode the prostate specific antigen (PSA).
 CC The detection of PSA mRNA in peripheral blood is associated with
 CC metastatic prostate cancer. Detection of PSA mRNA in the bloodstream
 CC indicates that prostate cells are circulating in the blood and confirms
 CC diagnosis of cancer. Circulating prostate cells also indicate a risk of a
 CC secondary tumour or bone metastatic anchoring. Detection of the PSA mRNA
 CC after prostatectomy or radiotherapy indicates a risk that the prostate
 CC cancer has spread and that the surgery and radiotherapy was not
 CC effective. PCR primers AAT92971-73 were used for the monitoring and
 CC diagnosis of patients with prostate cancer. The method comprises the
 CC detection of PSA mRNA by reverse transcriptase polymerase chain reaction
 CC (RT-PCR)
 XX
 SQ Sequence 208 BP; 29 A; 62 C; 73 G; 44 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 9,928-05 Length: 208
 Score: 147.00 Matches: 22
 Percent Similarity: 75.00% Conservative: 11
 Best Local Similarity: 50.00% Mismatches: 11
 Query Match: 11.69% Indels: 0
 DB: 2 Gaps: 0
 US-09-856-320A-2_COPY_54_282 (1-229) x AAT92975 (1-208)
 QY 1 IleIleLySgLyPheLcUcYsLysProHisSerGlnProTrpGlnAlaAlaLeuPheGlu 20
 DB 49 ATTGTGGAGGCTGGAGTGGCAGAGCATTCACCAACCTGGCAGGTGTTGGCCCTCT 108
 QY 21 LysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAla 40
 DB 109 CATTGGAGGCGCATCTGGCGCGGTTCGTGTCGCCACCCAGTGGGTCTCACAGTCTCC 168
 QY 41 HisCysLeuLys 44
 DB 169 CACTGCATCAGG 180
 RESULT 16
 AAT40854
 ID AAT40854 standard; cDNA; 225 BP.
 XX
 AC AAT40854;
 XX
 DT 16-MAR-1997 (first entry)
 XX
 DE Serine protease nFSP12-225 C-terminal fragment gene.
 XX
 KW flea; midgut; serine protease; nFSP12-225; recombinant vaccine;
 KW domestic animal; infestation; insecticide; protease-inhibitor;
 KW controlled release formulation; synergist; ss.
 XX
 OS Siphonaptera sp.
 XX
 XX Key Location/Qualifiers
 FH 1. .210
 CDS /*tag= b
 FT /*tag= "Serine protease nFSP12-69 fragment"
 FT 1. .207
 FT misc_feature /*tag= a

/note= "Sequence AAT40842 (claim 70)"
 FT
 XX WO9611706-A1.
 XX 25-APR-1996.
 XX 18-OCT-1995; 95WO-US014442.
 XX 18-OCT-1994; 94US-00326773.
 PR 07-JUN-1995; 95US-00482130.
 PR 07-JUN-1995; 95US-00484211.
 PR 07-JUN-1995; 95US-00485443.
 PR 07-JUN-1995; 95US-00485455.
 XX (HESK-) HESKA CORP.
 XX Grieve RB, Rushlow KE, Hunter SW, Frank GR, Stiegler GL, Heath A;
 PI Yamataka M, Arfsten A, Dale B;
 XX WPI; 1996-221762/22.
 DR P-PSDE; AAT40854.
 XX DNA encoding Flea serine protease and aminopeptidase - useful in vaccines
 PT to protect animals from flea infestation.
 XX
 PS Claim 70; Page 187; 241pp; English.
 XX
 CC This sequence, nFSP12-225, encodes a C-terminal fragment of a flea midgut
 CC serine protease, PfSP12-69, and has been isolated from a flea cDNA
 CC library by PCR using primers AAT40862-63 and hybridisation with probe
 CC AAT40866, based on conserved serine protease sequences. The sequence
 CC contains a stop codon, and contains C-terminal sequence AAT40842. An N-
 CC terminal fragment of the protease gene, nFSP12-144 (AAT40836), has also
 CC been isolated. The sequence may be used to produce a recombinant vaccine
 CC for protection of domestic animals from flea infestation, or in isolation
 CC of protease-inhibitors which may be used in controlled release
 CC formulations to reduce the flea burden on and around the animal. The
 CC inhibitors may be included in insecticidal compositions to increase
 CC efficacy of other active compounds, by reducing proteolytic activity in
 CC the flea midgut
 XX
 SQ Sequence 225 BP; 67 A; 43 C; 48 G; 67 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 0.00011 Length: 225
 Score: 147.00 Matches: 31
 Percent Similarity: 75.51% Conservative: 6
 Best Local Similarity: 63.27% Mismatches: 10
 Query Match: 11.69% Indels: 3
 DB: 2 Gaps: 2
 US-09-856-320A-2_COPY_54_282 (1-229) x AAT40854 (1-225)
 QY 175 LysAspSerCysGlnGlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGly 194
 DB 43 AAGGGTGCATGTAAGGGTGATTCGGTGGCCCTTAGTCATCAATGGACAACTTCATGGA 102
 QY 195 IleIleSerTrpGlyGlnAspProCysAlaIleThrArgLysProGlyValThrLys 214
 DB 103 ATTCTTCTCGGGGC---ATTCTTGGCTGT---CGCAAGCCTGATGATTACAGA 155
 QY 215 ValCysLysTrpValAspTrpIleGln 223
 DB 156 GTTTCTCATATTGTCGATTGATTAA 182
 RESULT 17
 AAV04599
 ID AAV04599 standard; DNA; 225 BP.
 XX
 AC AAV04599;
 XX
 DT 25-MAR-2003 (revised)
 DT 02-JUL-1998 (first entry)

XX Flea serine protease DNA sequence SEQ ID NO:131.

XX DE

XX KW Flea; Siphonaptera; protease; vaccine; prophylaxis; infestation;

XX KW immunoglobulin protease; larvae; host animal; ss.

XX OS Siphonaptera.

XX PN WO9740058-A1:

XX PD 30-OCT-1997.

XX PF 24-APR-1997; 97WO-US006121.

XX PR 24-APR-1996; 96US-00639075.

XX PR 15-NOV-1996; 96US-00749699.

XX PR 04-APR-1997; 97US-00429459.

XX PA (HESK-) HESKA CORP.

XX PI Grieve RB, Rushlow KE, Hunter SM, Frank GR, Steigler GL;

XX PI Gaines RJ, Silver G;

XX PI WPI; 1998-076762/07.

XX DR New flea protease genes and proteins - used in vaccine compositions for

XX PT the prophylaxis and treatment of flea infestation, especially in cats or

XX PT dogs.

XX PS Claim 1; Page 262; 318pp; English.

XX CC The present sequence is a DNA sequence from a novel flea serine protease.

XX CC The protease, its mimetopes, antibodies (Ab) and inhibitors of the

XX CC protein, as well as the DNA encoding the protein, may all be used in

XX CC therapeutic compositions to reduce flea protease activity (especially

XX CC immunoglobulin protease) and so reduce flea infestation, especially in

XX CC cats or dogs. Alternatively, flea larvae may ingest the faeces of adult

XX CC fleas which comprises anti-protease antibodies produced by a host animal

XX CC in response to administration of the protein. Therapeutic compositions

XX CC may further comprise a compound that reduces haematophagous ectoparasite

XX CC burden by a method other than by reducing flea immunoglobulin protease

XX CC activity. The novel flea DNA encoding the protein can also be used to

XX CC produce recombinant protein, and fragments of it are used as probes and

XX CC primers for identification and isolation of related sequences, also as

XX CC antisense, triplex-forming agents and ribozymes for inhibition of the

XX CC synthesis of the protein. Ab are also useful for screening expression

XX CC libraries, to purify the protein and to target cytotoxins to fleas.

XX CC (Updated on 25-MAR-2003 to correct PI field.)

XX SQ Sequence 225 BP; 67 A; 43 C; 48 G; 67 T; 0 U; 0 Other;

Alignment Scores:			
Pred. No.:	0.00011	Length:	225
Score:	147.00	Matches:	31
Percent Similarity:	75.51%	Conservative:	6
Best Local Similarity:	63.27%	Mismatches:	10
Query Match:	11.69%	Indels:	3
DB:	2	Gaps:	2

US-09-856-320A-2_COPY_54_282 (1-229) x AAV04599 (1-225)

QY 175 lysAspSerCysGlnGlyAspSerGlyGlyProLeuValCysAenGlnSerLeuGlnGly 194

DB 43 AAGGGTGATGTAAGGGTGATTCGGGTGGCCCTTAGTCATCATGACCAACTTCATGGA 102

QY 195 lleIleSerTrpGlyGlnAspProCysAlaIleThrArgLysProGlyValTyrThrLys 214

DB 103 ATTGTTCCTGGGCGC---ATTCTTGGCGCTGT----CGCAAGCCTGATGATTCCACAGA 155

QY 215 ValCysLysTyrValAspTrpIleGln 223

DB 156 GTTCTCTCATTATGCGATTGATTAA 182

RESULT 18	
AAC90862	
ID AAC90862 standard; cDNA; 225 BP.	
XX	
XX AAC90862;	
XX	
XX 19-MAR-2001 (first entry)	
XX	
XX Flea serine protease nFSP12-225 nucleotide sequence #100.	
XX	
XX Flea; cat flea; serine protease; aminopeptidase; cysteine protease;	
KW flea infestation; proteolytic; insecticide; vaccine; cat; dog; dog flea;	
KW Ctenocephalides felis; Ctenocephalides canis; Pulex irritans;	
KW ectoparasite; ss.	
XX	
OS Ctenocephalides felis.	
XX	
XX US6150125-A.	
PN	
XX 21-NOV-2000.	
PD	
XX	
XX 24-APR-1996; 96US-00639075.	
PF	
XX 13-DEC-1991; 91US-00806482.	
FR	
XX 18-OCT-1994; 94US-00326773.	
FR	
XX 07-JUN-1995; 95US-00482130.	
FR	
XX 07-JUN-1995; 95US-00484211.	
FR	
XX 07-JUN-1995; 95US-00485443.	
FR	
XX 07-JUN-1995; 95US-00485455.	
FR	
XX 15-AUG-1997; 97WO-US014442.	
XX	
XX (HESK-) HESKA CORP.	
XX	
PA Gaines PJ, Silver G, Rushlow KE, Hunter SW, Frank GR;	
PI Stiegler GL, Grieve RB;	
XX	
XX WPI: 2001-136374/14.	
DR P-PSDB; AAB50606.	
DR	
XX	
XX New isolated flea proteins with proteolytic activity, useful for	
PT preventing and reducing flea infestations in mammals especially cats and	
PT dogs.	
XX	
PS Claim 4; Col 161-162; 150pp; English.	
XX	
XX The present invention describes isolated flea serine protease,	
CC aminopeptidase and cysteine protease proteins (I). Also described is a	
CC method for identifying a compound (II) capable of inhibiting flea	
CC protease activity comprising: (a) contacting (I) with a protease	
CC substrate and a putative inhibitory compound, where (I) has proteolytic	
CC activity in the absence of the compound; and (b) determining if the	
CC compound inhibits protease activity by detecting cleavage of the protease	
CC substrates; where decreased cleavage of the protease substrate indicates	
CC an inhibitory compound. (I), nucleic acid molecules encoding (I), and	
CC antibodies immunospecific for (I) and (II) are useful for preventing and	
CC reducing flea infestations, particularly the species Ctenocephalides	
CC felis (cat fleas), Ctenocephalides canis (dog fleas) and Pulex irritans,	
CC in animals, preferably cats and dogs. They are also useful for reducing	
CC infestation by other ectoparasites, preferably mosquitoes, mites,	
CC sandflies, blackflies, ticks and Rhodnius. AAC90818 to AAC90913 and	
CC AAB50551 to AAB50644 represent sequences used in the exemplification of	
CC the present invention	
XX	
SQ Sequence 225 BP; 67 A; 43 C; 48 G; 67 T; 0 U; 0 Other;	
XX	
Alignment Scores:	
Pred. No.: 0.00011 Length: 225	
Score: 147.00 Matches: 31	
Percent Similarity: 75.51% Conservative: 6	
Best Local Similarity: 63.27% Mismatches: 10	
Query Match: 11.69% Indels: 3	
DB: 4 Gaps: 2	

US-09-856-320A-2_COPY_54_282 (1-229) x AAC09862 (1-225)

Qy 175 LysAspSerCysGlnGlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGly 194
 Db 43 AAGGTGATGTAAGGGTGAATTCGGTGGCCCTTAGTCATCAATGACAACTTCATGGA 102
 Qy 195 IleIleSerTrpGlyGlnAspProCysAlaIleThrArgLysProGlyValTyThrLys 214
 Db 103 ATTGTTCTCTGGGGC---ATTCTTCTGGCTGT---CGCAAGCTGTATTCACAAGA 155
 Qy 215 ValCysLysTyrrValAspTrpIleGln 223
 Db 156 GTTCTCATTATGTCGATTGGATTAAA 182

RESULT 19

AAT40847

ID AAT40847 standard; cDNA; 218 BP.

XX AAT40847;

XX 16-MAR-1997 (first entry)

XX Serine protease nfSP5-218 gene.

DE Flea; midgut; serine protease; nfSP5-218; recombinant vaccine;

KW domestic animal; infestation; insecticide; protease-inhibitor;

KW controlled release formulation; synergist; ss.

XX Siphonaptera sp.

XX Key Location/Qualifiers

FT CDS 3..218

FT /product= a

FT /tag= "serine protease PfSP5-72"

FT misc_feature 42..203

FT /tag= b

FT /note= "nfSP5-159 (AAT40823, claim 70)"

FT WO9611706-A1.

PN 25-APR-1996.

PD 18-OCT-1995;

PF 95WO-US014442.

XX 18-OCT-1994;

PR 94US-00326773.

PR 07-JUN-1995;

PR 95US-00482130.

PR 07-JUN-1995;

PR 95US-00484211.

PR 07-JUN-1995;

PR 95US-00485443.

PR 07-JUN-1995;

PR 95US-00485455.

XX (HESK-) HESKA CORP.

PA Grieve RB, Rushlow KE, Hunter SW, Frank GR, Stiegler GL, Heath A;

XX Yamanaka M, Arifsten A, Dale B;

PI WPI; 1996-221762/22.

XX P-PSDB; AAW01202.

DR DNA encoding Flea serine protease and aminopeptidase - useful in vaccines

XX to protect animals from flea infestation.

PI Claim 70; Page 176; 241pp; English.

XX This sequence (nfSP5-218) encodes a flea midgut serine protease partial

CC sequence (PfSP5-72) and has been isolated from a flea cDNA library by

CC PCR using primers AAT40862-63 and hybridisation with probe AAT40866,

CC based on conserved serine protease sequences. The sequence contains

CC sequence AAT40823 (nfSP5-159), which spans 2 conserved serine protease

CC sequences, and an additional partial sequence is given in AAT40846 (nfSP5

CC -157). The sequence may be used to produce a recombinant vaccine for

CC protection of domestic animals from flea infestation, or in isolation of

CC protease-inhibitors which may be used in controlled release formulations

CC to reduce the flea burden on and around the animal. The inhibitors may be

CC included in insecticidal compositions to increase efficacy of other
 CC active compounds, by reducing proteolytic activity in the flea midgut
 XX Sequence 218 BP; 60 A; 48 C; 52 G; 58 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0.00013 Length: 218
 Score: 146.00 Matches: 30
 Percent Similarity: 59.72% Conservative: 13
 Best Local Similarity: 41.67% Mismatches: 23
 Query Match: 11.61% Indels: 6
 DB: 2 Gaps: 3

US-09-856-320A-2_COPY_54_282 (1-229) x AAT40847 (1-218)

Qy 115 ValThrAlaGlyThrSerCysLeuIleSerGlyTrpGlySerThrSerSer-----Pro 132
 Db 12 TTAACACCTCGAACTATGTGCACTGTACTGGATGGGATCAACTGGATCTGGTGTCCA 71
 Qy 133 GlnLeuArgLeuProHisThrIleuA-CysAlaAsnIleThrIleIleGluHisGlnLys 152
 Db 72 -----ATTACAAATGTTCTACAAGAGTTCGAAGTTCCATTATCGACTTCAACACC 122
 Qy 153 CysGluAsnAlaTyrrProGlyAsnIleThrAspThrMetValCysAlaSer---ValGln 171
 Db 123 TGGCGAAATCCTACTCAACAGCTTAACGACCGATGTTCTGCGCTGGATTTTGGGA 182
 Qy 172 GluGlyGlyLysAspSerCysGlnGlyAspSerGly 183
 Db 183 ATTGGTGTAAAGACGCTTGCCCAAGCGACTCCGGA 218

RESULT 20

AAV04590

ID AAV04590 standard; DNA; 218 BP.

XX AAV04590;

XX 25-MAR-2003 (revised)

DT 02-JUL-1998 (first entry)

XX Flea serine protease DNA sequence SEQ ID NO:117.

DE Flea; Siphonaptera; protease; vaccine; prophylaxis; infestation;

KW immunoglobulin protease; larvae; host animal; ss.

XX Siphonaptera.

XX WO9740058-A1.

XX 30-OCT-1997.

XX 24-APR-1997; 97WO-US006121.

XX 24-APR-1996; 96US-00639075.

PR 15-NOV-1996; 96US-00749699.

PR 04-APR-1997; 97US-0042945P.

XX (HESK-) HESKA CORP.

XX Grieve RB, Rushlow KE, Hunter SW, Frank GR, Steigler GL;

PI Gaines PJ, Silver G;

XX WPI; 1998-076762/07.

XX New flea protease genes and proteins - used in vaccine compositions for

CC the prophylaxis and treatment of flea infestation, especially in cats or

CC dogs.

XX Claim 1; Page 253; 318pp; English.

CC The present sequence is a DNA sequence from a novel flea serine protease.

CC The protease, its mimetopes, antibodies (Ab) and inhibitors of the

CC protein, as well as the DNA encoding the protein, may all be used in

therapeutic compositions to reduce flea protease activity (especially immunoglobulin protease) and so reduce flea infestation, especially in cats or dogs. Alternatively, flea larvae may ingest the faeces of adult fleas which comprises anti-protease antibodies produced by a host animal in response to administration of the protein. Therapeutic compositions may further comprise a compound that reduces haematophagous ectoparasite burden by a method other than by reducing flea immunoglobulin protease activity. The novel flea DNA encoding the protein can also be used to produce recombinant protein, and fragments of it are used as probes and primers for identification and isolation of related sequences, also as antisense, triplex-forming agents and ribozymes for inhibition of the synthesis of the protein. Ab are also useful for screening expression libraries, to purify the protein and to target cytotoxins to fleas.

(Updated on 25-MAR-2003 to correct PI field.)

Sequence 218 BP; 60 A; 48 C; 52 G; 58 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 0.00013 Length: 218
 Score: 146.00 Matches: 30
 Percent Similarity: 59.72% Conservativeness: 13
 Best Local Similarity: 41.67% Mismatches: 23
 Query Match: 11.61% Indels: 6
 DB: 2 Gaps: 3

US-09-856-320A-2_COPY_54_282 (1-229) x AAV04590 (1-218)

QY 115 ValThrAlaGlyThrSerCysLeuIleSerGlyTrpGlySerThrSerSer-----Pro 132
 Db 12 TTAACACCTGGAACTATGTCACCTGTTACTGGAATGGGATCAACTGATCGTGGTCCCA 71
 QY 133 GlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIleIleGluHisGlnLys 152
 Db 72 -----ATTACAAATGTTCTACAGAGTCAAGTTCCTCAATTTATCGACTTCAACACC 122
 QY 153 CysGluAsnAlaTyPrOGlyAsnIleThrAspThrMetValCysAlaSer---ValGln 171
 Db 123 TGCAGAAATCCTACTACACAGCTTAACGACCGATGTTCTGCGCTGGATTTTGGGA 182
 QY 172 GluGlyClyLysAspSerCysGlnGlyAspSerGly 183
 Db 183 ATTGGTGTGAAGACGCTTCCCAAGGCGACTCCGGA 218

RESULT 21

AAC90855
 ID AAC90855 standard; CDNA; 218 BP.

XX
 AC AAC90855;
 XX
 DT 19-MAR-2001 (first entry)
 XX
 DE Flea serine protease nFSP5-218 nucleotide sequence #86.
 XX
 KW Flea; cat flea; serine protease; aminopeptidase; cysteine protease;
 KW flea infestation; proteolytic; insecticide; vaccine; cat; dog; flea;
 KW Ctenocephalides felis; Ctenocephalides canis; Pulex irritans;
 KW ectoparasite; ss.

Ctenocephalides felis.

US6150125-A.

XX 21-NOV-2000.

XX 24-APR-1996; 96US-00639075.

XX 13-DEC-1991; 91US-00806482.

XX 18-OCT-1994; 94US-00326773.

XX 07-JUN-1995; 95US-00482130.

XX 07-JUN-1995; 95US-00484211.

XX 07-JUN-1995; 95US-00485443.

XX 07-JUN-1995; 95US-00485455.

XX 15-AUG-1997; 97NO-US014442.

XX (HESK-) HESKA CORP.
 PA
 XX
 PI Gaines PJ, Silver G, Rushlow KE, Hunter SW, Frank GR;
 PI Stiegler GL, Grieve RB;
 DR WPI; 2001-136374/14.
 DR P-PSDB; AAB50599.

PT New isolated flea proteins with proteolytic activity, useful for preventing and reducing flea infestations in mammals especially cats and dogs.

XX Claim 4; Col 143-144; 150pp; English.

XX
 CC The present invention describes isolated flea serine protease, aminopeptidase and cysteine protease proteins (I). Also described is a method for identifying a compound (II) capable of inhibiting flea protease activity comprising: (a) contacting (I) with a protease substrate and a putative inhibitory compound, where (I) has proteolytic activity in the absence of the compound; and (b) determining if the compound inhibits protease activity by detecting cleavage of the protease substrates, where decreased cleavage of the protease substrate indicates an inhibitory compound. (I), nucleic acid molecules encoding (I), and antibodies immunospecific for (I) and (II) are useful for preventing and reducing flea infestations, particularly the species Ctenocephalides felis (cat fleas), Ctenocephalides canis (dog fleas) and Pulex irritans, in animals, preferably cats and dogs. They are also useful for reducing infestation by other ectoparasites, preferably mosquitoes, midges, sandflies, blackflies, ticks and Rhodnius. AAC90818 to AAC90913 and AAB50551 to AAB50644 represent sequences used in the exemplification of the present invention

XX Sequence 218 BP; 60 A; 48 C; 52 G; 58 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0.00013 Length: 218
 Score: 146.00 Matches: 30
 Percent Similarity: 59.72% Conservativeness: 13
 Best Local Similarity: 41.67% Mismatches: 23
 Query Match: 11.61% Indels: 6
 DB: 2 Gaps: 3

US-09-856-320A-2_COPY_54_282 (1-229) x AAC90855 (1-218)

QY 115 ValThrAlaGlyThrSerCysLeuIleSerGlyTrpGlySerThrSerSer-----Pro 132
 Db 12 TTAACACCTGGAACTATGTCACCTGTTACTGGAATGGGATCAACTGATCGTGGTCCCA 71

QY 133 GlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIleIleGluHisGlnLys 152
 Db 72 -----ATTACAAATGTTCTACAGAGTCAAGTTCCTCAATTTATCGACTTCAACACC 122

QY 153 CysGluAsnAlaTyPrOGlyAsnIleThrAspThrMetValCysAlaSer---ValGln 171
 Db 123 TGCAGAAATCCTACTACACAGCTTAACGACCGATGTTCTGCGCTGGATTTTGGGA 182

QY 172 GluGlyClyLysAspSerCysGlnGlyAspSerGly 183

Db 183 ATTGGTGTGAAGACGCTTCCCAAGGCGACTCCGGA 218

RESULT 22

ABK48911
 ID ABK48911 standard; DNA; 137 BP.

XX AC ABK48911;

XX 02-JUL-2002 (first entry)

XX Novel human kallikrein KLK15, exon 4.

KW Kallikrein; KLK15; cancer; prostate cancer; colon cancer; kidney cancer; testicular cancer; thyroid disorder; chromosome 19q13.3-q13.4; ds.

OS Homo sapiens.
XX
PN WO200192581-A2.
XX
XX PD 06-DEC-2001.
XX
XX PF 29-MAY-2001; 2001WO-US017756.
XX
XX PR 26-MAY-2000; 2000US-0207484P.
XX
XX PA (CORI-) CORIXA CORP.
XX
XX PI Algate PA, Harlocker SL, Jones R;
XX
XX DR WPI; 2002-122075/16.
XX
XX PT Composition for therapy and diagnosis of ovarian cancer comprising
PT polypeptide of an ovarian tumor polypeptide, polynucleotide encoding
PT polypeptide, antibody specific to polypeptide or T cell expressing
PT polypeptide.
XX
PS Claim 1; SEQ ID NO 3234; 489pp; English.
XX

The present invention describes a composition (I) comprising: carriers and immunostimulants; and a polypeptide (II) of an ovarian tumour polypeptide encoded by a polynucleotide (III) having a cDNA sequence (S1) from the 10912 nucleotide sequences as given in ABL77023 to ABL87934, (III) encoding (II) having a sequence (S2), a T cell population of (II), or antigen presenting cells that express (II). (I) has cytostatic activity. An oligonucleotide (IV) that hybridises to (S1) can be used for detecting ovarian cancer in a patient's biological sample preferably serum or ovarian tissue. The method comprises contacting a biological sample from a patient with (IV), detecting the amount of polynucleotide hybridising to (IV) and comparing the amount to a predetermined cutoff value and thereby detecting ovarian cancer in the patient, where the amount of polynucleotide hybridising to (IV) is detected preferably by polymerase chain reaction (PCR). (I) comprising (III) and/or (II) is useful for stimulating and/or expanding T cells specific for an ovarian tumour protein comprising contracting T cells with (III) or (II). (III) is useful in design and preparation of ribozyme molecules for inhibiting expression of the tumour polypeptides and proteins in tumour cells; and CC to isolate a full length gene from a suitable library e.g., a tumour cDNA library using well known techniques

XX SQ Sequence 163 BP; 36 A; 40 C; 51 G; 36 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0.000714 Length: 163
Score: 136.00 Matches: 25
Percent Similarity: 64.81% Conservative: 10
Best Local Similarity: 46.30% Mismatches: 19
Query Match: 10.81% Indels: 0
DB: Gaps: 0

US-09-856-320A-2_COPY_54_282 (1-229) x ABL80256 (1-163)

Qy 176 AspSerCysGlnAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyile 195
Db 163 AACCTCCCAAGGGGAATTCCTGGGGCCCTTTGGTCCCTCATGGCTCTCGACGAGGCC 104
Qy 196 IleserTrpGlyGlnAspProCysAlaIleThrArgLysProGlyValTyThrLysVal 215
Db 103 GTGTCTGGGGATTATACCCTTGCCCGCCGACACAGACCGGTTTTCTACAGAACCTC 44
Qy 216 CysLysTyrrValAspTrpIleGlnGluThrMetLysAsnAsn 239
Db 43 TGCAAGTTTCCAAAGTGGATCCAGGAACCATCCAGGCCAAC 2

RESULT 24
RAQ31930
ID RAQ31930 standard; DNA; 205 BP.
XX AC RAQ31930;

OS Homo sapiens.
XX
PN WO200214485-A2.
XX
XX PD 21-FEB-2002.
XX
XX PF 10-AUG-2001; 2001WO-CA001141.
XX
XX PR 11-AUG-2000; 2000US-0224853P.
XX
XX PA (MOUN) MOUNT SINAI HOSPITAL.
XX
XX PI Yousef OM, Diamandis EP;
XX
XX DR WPI; 2002-329575/36.
XX

Novel kallikrein protein, KLK15 and nucleic acid molecule encoding the protein useful for diagnosing, monitoring and treating thyroid disorders and cancer, particularly prostate, colon, kidney and testicular cancer.

Claim 3; Page 62; 67pp; English.

The invention describes an isolated kallikrein protein (I) (KLK15) and splice variants of (I). (I) is useful for identifying a substance which associates with (I) and for evaluating a compound for its ability to modulate the biological activity of (I). An anti-(I) antibody labelled with a detectable substance is useful to detect KLK15 polypeptide in biological samples, tissues and cells. The antibody is also useful for monitoring the progression of cancer in an individual. (I) and the polynucleotide encoding it are useful for treatment of a condition mediated by KLK15 protein, in particular cancer (including prostate, colon, kidney and testicular cancer) and thyroid disorders. This sequence (located on chromosome 19q13.3-q13.4) represents exon 4 of the gene encoding the novel human kallikrein protein (see ABK48346) described in the invention

XX SQ Sequence 137 BP; 34 A; 36 C; 40 G; 27 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0.000572 Length: 137
Score: 136.00 Matches: 23
Percent Similarity: 70.45% Conservative: 8
Best Local Similarity: 52.27% Mismatches: 13
Query Match: 10.81% Indels: 0
DB: Gaps: 0

US-09-856-320A-2_COPY_54_282 (1-229) x ABK48911 (1-137)

Qy 136 LeuProHisThrIleuArgCysAlaAsnIleThrIlelleGluHisGlnLysCysGluAsn 155
Db 6 CTCGCCAGATACGTTGCATGTGTCACATCATCAGCATATCTCGACACATCTTGTGACAAG 65
Qy 156 AlaTyrrProGlyAsnIleThrAspThrMetValCysAlaIleThrValGlnGluGlyLys 175
Db 66 AGCTACCCAGGGCGCTGACAAACACCATTCGTTGTGTCAGGCGCGAGGCGAGCGCA 125
Qy 176 AspSerCysGln 179
Db 126 GAATCTGTGAG 137

RESULT 23
ABL80256/c
ID ABL80256 standard; cDNA; 163 BP.
XX AC ABL80256;
XX
XX DT 17-MAY-2002 (first entry)
XX
DE Human ovarian cancer related cDNA clone SEQ ID NO:3234.
XX
XX KW Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.
XX

```

XX DT 18-JAN-1993 (first entry)
XX DE Human scu-PA54 gene fragment M6 (O14-O16; O14A-O16A,B).
XX KW Single chain urokinase-type plasminogen activator; expression; plasmid;
XX KW ds.
XX OS Synthetic.
XX PN DR4101736-A.
XX PD 23-JUL-1992.
XX PF 22-JAN-1991; 91DE-04101736.
XX PR 22-JAN-1991; 91DE-04101736.
XX PA (CHEF ) GRUENENTHAL GMBH.
XX PI Steffens GJ, Guenzler WA, Flohe L, Brigelius-Flohe RE, Wolf B;
XX DR WPI; 1992-251111/31.
XX PT New recombinant peptide(s) contg. non-glycosylated scu-PA 54k sequence -
XX PT used as plasminogen activators, for treatment of infarction and to
XX PT prevent accumulation of platelets on thrombogenic surfaces.
XX PS Disclosure; Fig 6(c); 32pp; German.
XX CC The 3'- and 5'-end of the antisense strand overhangs the sense strand by
XX CC 4 bases. Synthetic fragments M4-M8 (AAQ25893 and AAQ31929-32) are used in
XX CC the prodn. of the scu-PA gene. The gene was used in plasmids for
XX CC expression of recombinant scu-PA43k (see AAR25395-404) in
XX CC Enterobacteriaceae (esp. E.coli). The plasmids also contain an operon
XX CC consisting of a regulatable promoter (see AAQ31933); a Shine- Dalgarno
XX CC sequence effective as ribosome-binding site; a start codon and 1 or 2
XX CC terminators
XX SQ Sequence 205 BP; 54 A; 59 C; 46 G; 46 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0.00118 Length: 205
Score: 135.00 Matches: 26
Percent Similarity: 58.82% Conservative: 14
Best Local Similarity: 38.24% Mismatches: 26
Query Match: 10.73% Indels: 2
DB: 2 Gaps: 1

US-09-856-320A-2_COPY_54_282 (1-229) x AAQ31930 (1-205)
QY 120 SerCysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThr 139
DB 2 TCITGCGAAATACCGCGTTTCGGTAAAGAAACTTACCGACTACCTGTACCGGAACAG 61
QY 140 LeuArgCysAlaAsnIleThrIleIleGluHisGlnLysCysGlu-----AsnAlaTyr 157
DB 62 CTGAATGACCGTTGTAAACTGATCTCTCCCGTGAATGCCAGCGCGCACTACTAC 121
QY 158 ProGlyAsnIleThrAspThrMetValCysAlaSerValGlnGlnGlyGlyLysAspSer 177
DB 122 GGTTCTGAAGTACCACCAAAATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 181
QY 178 CysGlnGlyAspSerGlyGlyPro 185
DB 182 TGCCAAAGGTGACTCTGTGTGTCCA 205

RESULT 25
AAx57985
ID AAx57985 standard; DNA; 227 BP.
XX AC AAx57985;
XX

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DT 19-JUL-1999 (first entry)
XX DE Human BS247 specific polynucleotide #3.
XX KW BS247; detection; diagnosis; breast cancer; atypical hyperplasia;
XX KW fibroadenoma; cystic breast disease; gene therapy; ss.
XX OS Homo sapiens.
XX PN WO9922027-A1.
XX PD 06-MAY-1999.
XX PF 28-OCT-1998; 98WO-US022906.
XX PR 28-OCT-1997; 97US-0063431P.
XX PR 28-OCT-1997; 97US-00968838.
XX PA (ABBO ) ABBOTT LAB.
XX PI Billig-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
XX PI Granados EN, Hodges SC, Klass MK, Kratochvil JD, Russell JC;
XX PI Stroupe SD, Yu H;
XX DR WPI; 1999-312977/26.
XX PT Breast tissue derived cDNA contig and consensus polypeptide sequence.
XX PS Claim 1; Page 104; 112pp; English.
XX CC This sequence is a BS247 specific polynucleotide. The invention relates
XX CC to a method of detecting the presence of a target BS247 polynucleotide,
XX CC especially mRNA, in a test sample. BS247 polynucleotides are derived from
XX CC breast tissue. The polynucleotides, polypeptides or antibodies are useful
XX CC for providing information leading to the detection, diagnosis, staging,
XX CC monitoring, prognosis, in vivo imaging, prevention or treatment,
XX CC determining predisposition to, diseases and conditions of the breast,
XX CC such as breast cancer, atypical hyperplasia, fibroadenoma and cystic
XX CC breast disease. Drug treatment or gene therapy for breast cancer, can be
XX CC based on these identified gene sequences and the efficacy of any
XX CC particular therapy can be monitored. The BS247-derived reagents are
XX CC advantageous for detection of breast cancer due to their specificity. The
XX CC reagents also provide an alternative, non-surgical diagnostic method
XX CC capable of detecting early stage breast disease, such as cancer
XX SQ Sequence 227 BP; 55 A; 80 C; 42 G; 50 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0.00149 Length: 227
Score: 134.50 Matches: 30
Percent Similarity: 56.41% Conservative: 14
Best Local Similarity: 38.46% Mismatches: 29
Query Match: 10.69% Indels: 5
DB: 2 Gaps: 2

US-09-856-320A-2_COPY_54_282 (1-229) x AAx57985 (1-227)
QY 38 ThrAlaAlaHisCysLeuLysProArgTyrIleValHisLeuGlyGlnHisAsnLeuGln 57
DB 2 ACGGCGCGCCACTGCAGAGAAAGTTTTCAGAGTCCGTCTCGGCCACTACTCCCTGTCA 61
QY 58 Lys---GluGluGlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGly 76
DB 62 CCAGTTTATGATCTGGCGAGCAGATGTTCCAGGGGTCAATCCATCCCCACCTGGC 121
QY 77 PheAsnAsnSerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAla 96
DB 122 TACTCC-----CACCCTGGCCACTCTTAACGACCTCATGCTCATCAAACTGAAC 169
QY 97 SerProValSerIleThrTrpAlaValArgProLeuThrLeuSerSerArgCys 114
DB 170 AGAAGAATTGCTCCCACTAAAGATGTCAGACCCATCAACGCTCTCTCTATTGT 223

```

RESULT 26

AAZ89009
ID AAZ89009 standard; DNA; 180 BP.
XX
AC AAZ89009;
XX
DT 02-JUN-2000 (first entry)
XX
XX
DE Rat Factor IX DNA fragment.
XX
KW RAWIT; RNA amplification with in vitro translation; RAWTS; Factor IX;
KW RNA amplification with transcript sequencing; rat; ss.
XX
OS Rattus sp.
XX
XX
PN US6027913-A.
XX
XX
PD 22-FEB-2000.
XX
XX
PF 27-DEC-1994; 94US-00399855.
XX
PR 28-JAN-1988; 88US-00149312.
PR 24-JUL-1989; 89US-00385013.
PR 12-NOV-1993; 93US-00151461.
XX
PA (SOMM/) SOMMER S S.
XX
XX
PI Sommer SS;
XX
XX
DR WPI; 2000-194830/17.
DR P-PSDB; AAY51619.
XX
XX
PT Producing polypeptides from nucleic acid sequences of interest using a
PT modified RAWIT (RNA amplification with in vitro translation) method.
XX
XX
PS Disclosure; Fig 4; 65pp; English.
XX
XX
CC This invention describes a novel modified RAWIT (RNA amplification with
CC in vitro translation) method, for synthesizing polypeptides encoded by
CC sequences of interest. The method generates a protein from an RNA
CC molecule and comprises (a) incubating the RNA with reverse transcriptase
CC to form cDNA; (b) amplifying the cDNA of step (a) to generate DNA copies
CC of the cDNA in the presence of at least 1 oligonucleotide primer which
CC contains an RNA promoter sequence; (c) transcribing the DNA generated
CC with an RNA polymerase to form RNA transcripts; and (d) translating the
CC RNA transcripts in vitro to generate the protein. This sequence encodes a
CC fragment of the rat Factor IX protein which is used to illustrate the
CC RAWTS (RNA amplification with transcript sequencing) method of the
CC invention
XX
SQ Sequence 180 BP; 62 A; 30 C; 41 G; 47 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0.00186 Length: 180
Score: 132.00 Matches: 24
Percent Similarity: 58.33% Conservative: 11
Best Local Similarity: 40.00% Mismatches: 23
Query Match: 10.49% Indels: 2
DB: 3 Gaps: 1

US-09-856-320A-2_COPY_54_282 (1-229) x AAZ89009 (1-180)

QY 21 LysThrArgLeuLeuCysGlyAlaThrLeuLeuAlaProArgTrpLeuLeuThrAlaAla 40
DB 1 AAAGTTGATGCATCTCTGTGGAGCGGCATCATTAATGAAATAATGGAATGTAATGCTGCC 60
QY 41 HisCysLeuLysPro-----ArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLys 58
DB 61 CACTGTCTTAACCTGGTGATAAAATGAGTTGTGCTGGTGAACATAATATTGATGAG 120
QY 59 GluGluGlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsn 78
DB 121 AAGGAAGACACAGAAAGAGAGAAATGTGATTGGAACATATCCCTCATCCACGATCAAT 180

RESULT 27

AAZ89011
ID AAZ89011 standard; DNA; 180 BP.
XX
AC AAZ89011;
XX
DT 02-JUN-2000 (first entry)
XX
XX
DE Rabbit Factor IX DNA fragment.
XX
KW RAWIT; RNA amplification with in vitro translation; RAWTS; Factor IX;
KW RNA amplification with transcript sequencing; rabbit; ss.
XX
OS Oryctolagus cuniculus.
XX
XX
PN US6027913-A.
XX
XX
PD 22-FEB-2000.
XX
XX
PF 27-DEC-1994; 94US-00399855.
XX
PR 28-JAN-1988; 88US-00149312.
PR 24-JUL-1989; 89US-00385013.
PR 12-NOV-1993; 93US-00151461.
XX
PA (SOMM/) SOMMER S S.
XX
XX
PI Sommer SS;
XX
XX
DR WPI; 2000-194830/17.
DR P-PSDB; AAY51620.
XX
XX
PT Producing polypeptides from nucleic acid sequences of interest using a
PT modified RAWIT (RNA amplification with in vitro translation) method.
XX
XX
PS Disclosure; Fig 4; 65pp; English.
XX
XX
CC This invention describes a novel modified RAWIT (RNA amplification with
CC in vitro translation) method, for synthesizing polypeptides encoded by
CC sequences of interest. The method generates a protein from an RNA
CC molecule and comprises (a) incubating the RNA with reverse transcriptase
CC to form cDNA; (b) amplifying the cDNA of step (a) to generate DNA copies
CC of the cDNA in the presence of at least 1 oligonucleotide primer which
CC contains an RNA promoter sequence; (c) transcribing the DNA generated
CC with an RNA polymerase to form RNA transcripts; and (d) translating the
CC RNA transcripts in vitro to generate the protein. This sequence encodes a
CC fragment of the rabbit Factor IX protein which is used to illustrate the
CC RAWTS (RNA amplification with transcript sequencing) method of the
CC invention
XX
SQ Sequence 180 BP; 55 A; 37 C; 41 G; 47 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0.00229 Length: 180
Score: 131.00 Matches: 22
Percent Similarity: 63.64% Conservative: 13
Best Local Similarity: 40.00% Mismatches: 18
Query Match: 10.41% Indels: 2
DB: 3 Gaps: 1

US-09-856-320A-2_COPY_54_282 (1-229) x AAZ89011 (1-180)

QY 26 CysGlyAlaThrLeuLeuAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysPro 45
DB 16 TGTGGAGTTCCATCGTTAATGAAATGTTGTAATGAGCCCTGATCAGCT 75
QY 46 -----ArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGluGluGlyCysGlu 63
DB 76 GGTGTAAATTAATCTGTTGTCAGGTGACATACATGAGAGCCAGACCTACAGAG 135
QY 64 GlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsn 78

Db 136 CAAAAGCGAATGTGATCCGTGCTATTCTTACCACGTTACAAT 180

RESULT 28

AAZ89008

ID AAZ89008 standard; DNA; 180 BP.

XX AAZ89008;

AC AAZ89008;

DT 02-JUN-2000 (first entry)

XX Murine Factor IX DNA fragment.

DE Murine Factor IX DNA fragment.

XX RAWIT; RNA amplification with in vitro translation; RAWTS; Factor IX;

KW RNA amplification with transcript sequencing; mouse; ss.

XX Mus sp.

OS US6027913-A.

XX 22-FEB-2000.

PD 27-DEC-1994; 94US-00399855.

PF 28-JAN-1988; 88US-00149312.

XX 24-JUL-1989; 89US-00385013.

PR 12-NOV-1993; 93US-00151461.

XX (SOMM/) SOMMER S S.

FA Sommer SS;

XX WPI; 2000-194830/17.

XX P-PSDB; AAY51618.

DR Producing polypeptides from nucleic acid sequences of interest using a

PT modified RAWIT (RNA amplification with in vitro translation) method.

XX Disclosure; Fig 4; 65pp; English.

PS This invention describes a novel modified RAWIT (RNA amplification with

XX in vitro translation) method, for synthesizing polypeptides encoded by

CC sequences of interest. The method generates a protein from an RNA

CC molecule and comprises (a) incubating the RNA with reverse transcriptase

CC to form cDNA; (b) amplifying the cDNA of step (a) to generate DNA copies

CC of the cDNA in the presence of at least 1 oligonucleotide primer which

CC contains an RNA promoter sequence; (c) transcribing the DNA generated

CC with an RNA polymerase to form RNA transcripts; and (d) translating the

CC RNA transcripts in vitro to generate the protein. This sequence encodes a

CC fragment of the murine Factor IX protein which is used to illustrate the

CC RAWTS (RNA amplification with transcript sequencing) method of the

CC invention

XX SQ Sequence 180 BP; 63 A; 29 C; 40 G; 48 T; 0 U; 0 Other;

XX Alignment Scores:

Pred. No.: 0.00282 Length: 180

Score: 130.00 Matches: 24

Percent Similarity: 58.33% Conservative: 11

Best Local Similarity: 40.00% Mismatches: 23

Query Match: 10.33% Indels: 2

DB: Gaps: 3

US-09-856-320A-2_COPY_54_282 (1-229) x AAZ89008 (1-180)

QY 21 LysThrArgLeuLeuCysGlyAlaThrLeuLeuAlaProArgTrpLeuLeuThrAlaA 40

Db 1 AAGTTGATCATCTCTGTGAGTGCATCATTAATGAAATGATGTTACTGCTGCC 60

QY 41 HisCysLeuLysPro-----ArgTyrIleValHisLeuGlyClnHisAsnLeuGlnLys 58

Db 61 CACTGTCTTAAACCTGCTGATAAAATTTGAGTTGTTGCTGCAATATAACATTGATAAG 120

QY 59 GluGluGlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsn 78

Db 121 AAGGAAGACACAGAACAAAGGAGAAATGTGATTCCGAACATATCCCTCATCACCAGTACAAT 180

RESULT 29

AAZ89010

ID AAZ89010 standard; DNA; 180 BP.

XX AAZ89010;

AC AAZ89010;

DT 02-JUN-2000 (first entry)

XX Cavea sp. Factor IX DNA fragment.

DE Cavea sp. Factor IX DNA fragment.

XX RAWIT; RNA amplification with in vitro translation; RAWTS; Factor IX;

KW RNA amplification with transcript sequencing; guinea pig; ss.

XX Cavia sp.

OS US6027913-A.

XX 22-FEB-2000.

PD 27-DEC-1994; 94US-00399855.

PF 28-JAN-1988; 88US-00149312.

XX 24-JUL-1989; 89US-00385013.

PR 12-NOV-1993; 93US-00151461.

XX (SOMM/) SOMMER S S.

FA Sommer SS;

XX WPI; 2000-194830/17.

XX P-PSDB; AAY51619.

DR Producing polypeptides from nucleic acid sequences of interest using a

PT modified RAWIT (RNA amplification with in vitro translation) method.

XX Disclosure; Fig 4; 65pp; English.

PS This invention describes a novel modified RAWIT (RNA amplification with

XX in vitro translation) method, for synthesizing polypeptides encoded by

CC sequences of interest. The method generates a protein from an RNA

CC molecule and comprises (a) incubating the RNA with reverse transcriptase

CC to form cDNA; (b) amplifying the cDNA of step (a) to generate DNA copies

CC of the cDNA in the presence of at least 1 oligonucleotide primer which

CC contains an RNA promoter sequence; (c) transcribing the DNA generated

CC with an RNA polymerase to form RNA transcripts; and (d) translating the

CC RNA transcripts in vitro to generate the protein. This sequence encodes a

CC fragment of the guinea pig Factor IX protein which is used to illustrate the

CC RAWTS (RNA amplification with transcript sequencing) method of the

CC invention

XX SQ Sequence 180 BP; 64 A; 29 C; 41 G; 46 T; 0 U; 0 Other;

XX Alignment Scores:

Pred. No.: 0.00426 Length: 180

Score: 126.00 Matches: 22

Percent Similarity: 61.67% Conservative: 15

Best Local Similarity: 36.67% Mismatches: 21

Query Match: 10.17% Indels: 2

DB: Gaps: 3

US-09-856-320A-2_COPY_54_282 (1-229) x AAZ89010 (1-180)

QY 21 LysThrArgLeuLeuCysGlyAlaThrLeuLeuAlaProArgTrpLeuLeuThrAlaA 40

Db 1 GAAACTGAAGCATCTCTGTGAGTTCATCGTGAATGAAATGATGATGATGATGATGATG 60

QY 41 HisCysLeuLysPro-----ArgTyrIleValHisLeuGlyClnHisAsnLeuGlnLys 58

Db 61 CACTGTATTCTCCCTGGTATTAAATTTGAGTTGTTCCAGGTAAACATAATATTGAAAG 120

Qy 59 GluGluCysGluGlnThrArgThrAlaThrCluSerPheProHisProGlyPheAsn 78
Db 121 AAGGAAGATACAGAGCAAGCGGAATGTGCACAGATTATTCTGCACCATAGTTACAAT 180

RESULT 30
ABV38446
ID ABV38446 standard; cDNA; 176 BP.
XX AC ABV38446;
XX DT 16-SEP-2002 (first entry)
XX DE Human prostate expression marker cDNA 38437.

XX KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX KW pharmacogenomic marker; gene; ss.
XX OS Homo sapiens.
XX PN WO200160860-A2.
XX PD 23-AUG-2001.
XX PF 20-FEB-2001; 2001WO-US005171.
XX PR 17-FEB-2000; 2000US-0183319P.
XX PR 16-MAR-2000; 2000US-0189862P.
XX PR 25-MAY-2000; 2000US-0207454P.
XX PR 09-JUN-2000; 2000US-0211314P.
XX PR 18-JUL-2000; 2000US-0219007P.
XX PR 13-DEC-2000; 2000US-0255281P.

XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX PI Schlegel R, Endege WO, Monahan JE;
XX DR WPI; 2001-662795/76.
XX PT Novel isolated nucleic acid molecule associated with cancerous state of
XX PT prostate cells and correlating with presence of prostate cancer, useful
XX PT for detecting presence of prostate cancer, stage of prostate cancer.

XX PS Claim 1; Page 7832; 11750pp; English.
XX CC The invention relates to an isolated nucleic acid molecule (I) comprising
XX CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
XX CC specification or its complement. (I) is useful for: (a) assessing whether
XX CC a patient is afflicted with prostate cancer; (b) monitoring the
XX CC progression of prostate cancer in a patient; (c) assessing the efficacy
XX CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
XX CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
XX CC (e) selecting a composition for inhibiting prostate cancer in a patient;
XX CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
XX CC determining whether prostate cancer has metastasized in a patient; (h)
XX CC assessing the aggressiveness or indolence of prostate cancer in a patient
XX CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker

XX SQ Sequence 176 BP; 29 A; 55 C; 61 G; 31 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 0.0051 Length: 176
Score: 127.00 Matches: 20
Percent Similarity: 72.22% Conservative: 6
Best Local Similarity: 55.56% Mismatches: 10
Query Match: 10.10% Indels: 0
DB: Gaps: 5

US-09-856-320A-2_COPY_54_282 (1-229) x ABV38446 (1-176)

Qy 6 GluCysLysProHisSerGlnProTrpGlnAlaLeuPheGluLysThrArgLeuLeu 25
Db 67 GACTGCAGCCGCACTCGCAGCCCTCGCAGCGCGCACTGTCATGCAAAACCAATTTTC 126

Qy 26 CysGlyAlaThrLeuLeuAlaProArgTrpLeuLeuThrAlaAlaHis 41
Db 127 TGCTCGGGGCTCTGGTGCATCCGCGAGTGGTGCTGTGACGGGCACAC 174

RESULT 31
ABX30380/c
ID ABX30380 standard; cDNA; 169 BP.
XX AC ABX30380;
XX DT 23-APR-2002 (first entry)
XX DE Human G-protein-coupled protease #150.

XX KW Human; ss; gene; G-protein-coupled protease; gene therapy; transgenic;
XX KW protease mediated disorder; proliferative disorder;
XX KW differentiative disorder; developmental disorder;
XX KW haematopoietic disorder.
XX OS Homo sapiens.
XX PN US6331427-B1.
XX PD 18-DEC-2001.
XX PF 26-MAR-1999; 99US-00280116.
XX PR 26-MAR-1999; 99US-00280116.

XX PA (MILL-) MILLENNIUM PHARM INC.
XX PI Robison KE;
XX DR WPI; 2002-129545/17.
XX PT New polynucleotides encoding protease homologs of the G-protein-coupled
XX PT protease family, useful in identifying agonists and antagonists for
XX PT diagnosis and treatment of protease mediated disorders.

XX PS Disclosure; Col 185-186; 246pp; English.
XX CC The invention relates to an isolated human protease nucleic acid molecule
XX CC comprising a nucleotide sequence of 546 base pairs, one of 268 fully
XX CC defined in the specification. Also disclosed are production of an
XX CC isolated polypeptide encoded by the nucleic acid, comprising introducing
XX CC the nucleic acid into a host cell and culturing under conditions to
XX CC express the protein from the nucleic acid, use of an antibody to detect
XX CC the encoded protein in a sample and to modulate its in vivo activity,
XX CC identifying agents that bind to the protein and identification of a
XX CC polynucleotide agent that modulates the expression of the nucleic acid or
XX CC its complement (i.e. gene therapy). The nucleic acid can be used to
XX CC identify an agent that modulates the expression or activity of the
XX CC nucleic acid, and can be used to isolate the protein. The nucleic acid
XX CC can be used in diagnostic assays for determining nucleic acid expression
XX CC as well as activity in the context of a biological sample (e.g., blood,
XX CC serum, cells, tissue) to determine whether an individual has a disease or
XX CC disorder, or is at risk of developing a disease or disorder, associated
XX CC with aberrant expression or activity of the nucleic acid. The nucleic
XX CC acid can be used to detect mutations in protease genes and gene
XX CC expression products such as mRNA. The nucleic acid can be used as
XX CC hybridisation probes to detect naturally-occurring genetic mutations in a
XX CC protease gene. The nucleic acid can be used in drug screening methods to
XX CC identify agonists and antagonists that can be used to diagnose and treat
XX CC such protease mediated disorders e.g., proliferative, differentiative,
XX CC developmental or haematopoietic disorders. The nucleic acid can be used
XX CC as probes, primers, in biological assays, to determine patterns of gene
XX CC expression, to design ribozymes and to construct transgenic animals. The
XX CC present sequence represents one of the 268 disclosed human G-protein-
XX CC coupled protease cDNA sequences

XX SQ Sequence 169 BP; 40 A; 48 C; 46 G; 35 T; 0 U; 0 Other;
Alignment Scores:

```

Pred. No.: 0.01 Length: 169
Score: 123.50 Matches: 29
Percent Similarity: 56.14% Conservative: 3
Best Local Similarity: 50.88% Mismatches: 24
Query Match: 9.82% Indels: 2
DB: 6 Gaps: 1

US-09-856-320A-2_COPY_54_282 (1-229) x ABA92483 (1-169)

QY 157 TyrProGlyAsnIleThrAspThrMetValCysAlaSerValGlnGlnGlyGlyLysAsp 176
Db 169 TACCCAGGAGATCACTAAAACATCTTCTGCTGGCTTCTGAGGGCGGAAGGAC 110
QY 177 SerCysGlnGlyAspSerGlyProLeuValCysAsnGlnSerLeuGlnGlyIle 196
Db 109 TCCTCCCGGGTGACTTTGGTGGCCCTTAGTCTCCAATGGACAACCCCGGGTGTTTT 50
QY 197 SerTyrGlyGlnAspProCysAlaIleThrArgLysProGlyValTyrThr 213
Db 49 TCCGGGGGTTATGG----TGTGCCAGAGAGAAACCTGGTTTCCACACC 3

RESULT 32
ABA92483
ID ABA92483 standard; DNA; 178 BP.
XX AC
XX ABA92483;
XX DT
XX 18-MAR-2002 (first entry)
XX DE
XX DNA oligonucleotide sequence SEQ ID NO:6.
XX KW
XX Detection; nucleic acid synthesis; identification; cancer; ss.
XX OS
XX Synthetic.
XX PN
XX WO200183817-A1.
XX PD
XX 08-NOV-2001.
XX PF
XX 25-APR-2001; 2001WO-JF003572.
XX PR
XX 01-MAY-2000; 2000JP-00132667.
XX PA
XX (BIKE ) EIKEN KAGAKU KK.
XX PI
XX Mori Y, Nagamine K;
XX WPI; 2002-075170/10.
XX DR
XX
XX PT
XX Detecting the product of an enzyme-based nucleic acid synthesizing
XX reaction, useful in gene analysis, diagnosis of cancer and other
XX diseases, and in identifying bacteria, comprises the formation of an
XX insoluble substance.
XX PS
XX Example 4; Page 18; 44pp; Japanese.
XX CC
XX The present invention describes a method for detecting the occurrence of
XX a nucleic acid synthesizing reaction during the synthesis of a nucleic
XX acid with an enzyme. The method comprises the use of an insoluble
XX substance formed in the reaction as an indication. The method can be used
XX for detecting the presence or absence of a nucleic acid synthesizing
XX reaction (especially a nucleic acid amplification reaction). The method
XX is useful in gene analysis, diagnosis of cancer and other diseases, and
XX in identifying bacteria. The present sequence represents an
XX oligonucleotide used in the exemplification of the present invention
XX SQ
XX Sequence 178 BP; 33 A; 56 C; 50 G; 39 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0.0119 Length: 178
Score: 123.00 Matches: 21
Percent Similarity: 63.46% Conservative: 12
Best Local Similarity: 40.38% Mismatches: 19
Query Match: 9.78% Indels: 0
DB: 6 Gaps: 0

US-09-856-320A-2_COPY_54_282 (1-229) x ABA01120 (1-178)

QY 23 ArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTyrLeuThrAlaAlaHisCys 42
Db 21 AGGGCAGTCTCGGGCGGTTCCTGGTGCAACCCCGAGTGGTCTTCACAGCTGCCACTGC 80
QY 43 LeuLysProArgTyrIleValHisLeuGlyGlnHisLeuGlnLysGluGlyCys 62
Db 81 ATCAGGAACAAAGCGGTGATCTTGGTGGTCGACACAGCCTGTTTCATCCTGAAGACACA 140
QY 63 GluGlnThrArgThrAlaThrGluSerPheProHis 74
Db 141 GGGCAGGTATTTTCAGTCCAGCCACAGCTTCACAC 176

RESULT 33
ABA01120
ID ABA01120 standard; DNA; 178 BP.
XX AC
XX ABA01120;
XX DT
XX C6-FEB-2002 (first entry)
XX DE
XX Human PSA nucleotide sequence.
XX KW
XX Human; nucleic acid synthesis; complementary chain synthesis; diagnosis;
XX ds.
XX OS
XX Homo sapiens.
XX PN
XX WO200177317-A1.
XX PD
XX 18-OCT-2001.
XX PF
XX 30-MAR-2001; 2001WO-JF002771.
XX PR
XX 07-APR-2000; 2000JP-00119399.
XX PA
XX (BIKE ) EIKEN KAGAKU KK.
XX PI
XX Notomi T, Nagamine K;
XX WPI; 2002-010907/01.
XX DR
XX
XX PT
XX Isothermal amplification of nucleic acids using double-stranded nucleic
XX acid as template to establish complementary chain synthesis reaction from
XX primer enabling base pairing in domain to be annealed, useful e.g. in
XX gene diagnosis.
XX PS
XX Example 1; Page 63; 75pp; Japanese.
XX CC
XX The invention relates to a method for synthesizing a nucleic acid using a
XX double-stranded nucleic acid as template and incubating under conditions
XX allowing the establishment of a complementary chain synthesis reaction.
XX The method uses an arbitrary primer to initiate the complementary chain
XX synthesis reaction. The method is particularly useful in gene and disease
XX diagnosis. It is a highly efficient and reaction specific method in which
XX no temperature variation is required. The present sequence is used in an
XX example illustrating the invention
XX SQ
XX Sequence 178 BP; 33 A; 56 C; 50 G; 39 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0.0119 Length: 178
Score: 123.00 Matches: 21
Percent Similarity: 63.46% Conservative: 12
Best Local Similarity: 40.38% Mismatches: 19
Query Match: 9.78% Indels: 0
DB: 6 Gaps: 0

US-09-856-320A-2_COPY_54_282 (1-229) x ABA01120 (1-178)

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QY 23 ArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCys 42
DB 21 AGGGCAGTCTGGGGGGTTCCTGTGTGCACCCCGAGTGGTCTCACAGCTGCCACTGC 80
QY 43 LeuLysProArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGluGluGlyCys 62
DB 81 ATCAGGAACAAAGCGTGTCTGTGTGGTGGCAGCCTGTTCATCTCTGAAGACACA 140
QY 63 GluGlnThrArgThrAlaThrGluSerPheProHis 74
DB 141 GGCCAGGTATTTTCAGTTCAGCCACAGCTTCACACAC 176
RESULT 34
ABS52622
ID ABS52622 standard; DNA; 178 BP.
AC ABS52622;
XX
XX
DT 15-NOV-2002 (first entry)
XX
DE Human DNA sequence used for polarised light detection.
XX
KW Human; polarised light; detection; amplified nucleic acid product; ds.
XX
XX Homo sapiens.
OS
FN JP2002186481-A.
PD 02-JUL-2002.
XX
XX 18-DEC-2000; 2000JP-00383650.
PF
XX 18-DEC-2000; 2000JP-00383650.
PR
XX (EIKE) EIKEN KAGAKU KK.
PA
XX WPI; 2002-594260/64.
DR
XX
XX
PT Detection method of amplified nucleic acid products with optical
PT Characteristic features using polarized light.
XX
XX
PS Example 1; Page 7; 11pp; Japanese.
CC
CC The present invention relates to the new application of polarised light
CC for detection method of amplified nucleic acid products. The invention
CC can be used for the detection of amplified nucleic acid products. The
CC invention is advantageous as it allows simple detection of amplified
CC nucleic acid products. The present nucleic acid sequence represents a
CC human DNA sequence that was used in the methods of the invention
XX
SQ Sequence 178 BP; 33 A; 56 C; 50 G; 39 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 0.0119 Length: 178
Score: 123.00 Matches: 21
Percent Similarity: 63.46% Conservative: 12
Best Local Similarity: 40.38% Mismatches: 19
Query Match: 9.78% Indels: 0
DB: 6 Gaps: 0
US-09-856-320A-2_COPY_54_282 (1-229) x ABS52622 (1-178)
QY 23 ArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCys 42
DB 21 AGGGCAGTCTGGGGGGTTCCTGTGTGCACCCCGAGTGGTCTCACAGCTGCCACTGC 80
QY 43 LeuLysProArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGluGluGlyCys 62
DB 81 ATCAGGAACAAAGCGTGTCTGTGTGGTGGCAGCCTGTTCATCTCTGAAGACACA 140
QY 63 GluGlnThrArgThrAlaThrGluSerPheProHis 74
DB 141 GGCCAGGTATTTTCAGTTCAGCCACAGCTTCACACAC 176

Db 141 GGCCAGGTATTTTCAGTTCAGCCACAGCTTCACACAC 176
RESULT 35
ABZ59354
ID ABZ59354 standard; DNA; 178 BP.
XX
XX
AC ABZ59354;
XX
XX
DT 15-APR-2003 (first entry)
XX
DE Loop-mediated isothermal amplification related oligonucleotide SEQ.1.
XX
KW Signal reduction; intercalator; gene analysis; disease diagnosis;
KW loop-mediated isothermal amplification; LAMP; ss.
XX
XX Synthetic.
OS
FN WO2002103053-A1.
PD 27-DEC-2002.
XX
XX 10-JUN-2002; 2002WO-JP005739.
PF
XX 18-JUN-2001; 2001JP-00183716.
PR
XX (EIKE) EIKEN KAGAKU KK.
PA
XX Tomita N, Mori Y;
FI
XX
DR WPI; 2003-175246/17.
XX
XX
PT Method for detecting double-stranded nucleic acids with reduced
PT background noise due to single-stranded nucleic acids, applicable in e.g.
PT gene analysis and disease diagnosis.
XX
PS Example 1; Page 22; 51pp; Japanese.
XX
CC
CC The present invention describes a method for reducing a signal
CC originating from an intercalator bonded to a single-stranded nucleic acid
CC (NA). The method comprises adding a compound reacting preferentially with
CC the intercalator bonded to the single-stranded (NA), in a mixture of the
CC double-stranded (NA) and the single-stranded (NA) to which the
CC intercalator is bonded. Also described: (1) a similar noise-reducing
CC method in which a compound having a higher binding strength to the single
CC -stranded (NA) than the intercalator but a lower binding strength to the
CC double-stranded (NA) than the intercalator bonded to the mixture to reduce such
CC signal originated from the intercalator bonded to the single-stranded
CC (NA); (2) treating the amplification product of a (NA) comprising: (a)
CC amplification of the (NA); adding intercalator to the reaction solution
CC after amplification; reducing signal originating from the intercalator
CC bonded to a single-stranded (NA) by the already- specified method; and
CC measuring fluorescence intensity of the reaction solution; or (b)
CC amplifying the (NA) in the presence of the intercalator; reducing signal
CC from the bond of the intercalator and single-stranded (NA); and measuring
CC fluorescence intensity of the reaction solution; or (c) amplifying the
CC (NA) in the presence of the intercalator and the compound having specific
CC binding strength to the (NA)s, and measuring fluorescence intensity; and
CC (3) kits for detecting double-stranded (NA)s containing the intercalator
CC and any of the specified compounds. The method is applicable in e.g. gene
CC analysis and disease diagnosis. The present sequence represents an
CC oligonucleotide related to loop-mediated isothermal amplification (LAMP),
CC which is used in an example from the present invention
XX
SQ Sequence 178 BP; 33 A; 56 C; 50 G; 39 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 0.0119 Length: 178
Score: 123.00 Matches: 21
Percent Similarity: 63.46% Conservative: 12
Best Local Similarity: 40.38% Mismatches: 19
Query Match: 9.78% Indels: 0
DB: 7 Gaps: 0

US-09-856-320A-2_COPY_54_282 (1-229) x ABZ59354 (1-178)

QY 23 ArgLeuLeuCysGlyAlaThrLeuLeuAlaProArgTrpLeuLeuThrAlaAlaHisCys 42
 Db 21 AGGCGAGTCTCGCGGGTGTCTGTGTCACCCCGAGTGGTCTTCACAGCTGCCACTGC 80
 QY 43 LeuLysProArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGluGluGlyCys 62
 Db 81 ATCAGGACAAACCGTGAATCTCTGGTGGCGACAGCTGTTCATCTGAGACACA 140
 QY 63 GluGlnThrArgThrAlaThrGluSerPheProHis 74
 Db 141 GGCAGGATTTTCAGGTCAGCCACAGCTTCACACAC 176

RESULT 36

AAZ89012

ID AAZ89012 standard; DNA; 180 BP.

AC AAZ89012;

DT 02-JUN-2000 (first entry)

DE Sheep Factor IX DNA fragment.

XX RAWIT; RNA amplification with in vitro translation; RAWTS; Factor IX;

KW RNA amplification with transcript sequencing; sheep; ss.

XX Ovis sp.

XX US6027913-A.

XX 22-FEB-2000.

XX 27-DEC-1994; 94US-00399855.

XX 28-JAN-1988; 88US-00149312.

XX 24-JUL-1989; 89US-00385013.

XX 12-NOV-1993; 93US-00151461.

XX (SOMM/) SOMMER S S.

XX Sommer SS;

XX WPI; 2000-194830/17.

XX P-PSDB; AAY51622.

XX Producing polypeptides from nucleic acid sequences of interest using a

XX modified RAWIT (RNA amplification with in vitro translation) method.

XX Disclosure; Fig 4; 65pp; English.

XX This invention describes a novel modified RAWIT (RNA amplification with

XX in vitro translation) method, for synthesizing polypeptides encoded by

XX sequences of interest. The method generates a protein from an RNA

XX molecule and comprises (a) incubating the RNA with reverse transcriptase

XX to form cDNA; (b) amplifying the cDNA of step (a) to generate DNA copies

XX of the cDNA in the presence of at least 1 oligonucleotide primer which

XX contains an RNA promoter sequence; (c) transcribing the DNA generated

XX with an RNA polymerase to form RNA transcripts; and (d) translating the

XX RNA transcripts in vitro to generate the protein. This sequence encodes a

XX fragment of the sheep Factor IX protein which is used to illustrate the

XX RAWTS (RNA amplification with transcript sequencing) method of the

XX invention

XX

SQ Sequence 180 BP; 64 A; 29 C; 39 G; 48 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0.0182 Length: 180

Score: 121.00 Matches: 22

Percent Similarity: 56.67% Conservative: 12

Best Local Similarity: 36.67% Mismatches: 24

Query Match: 9.62% Indels: 2

DB: 3 Gaps: 1

US-09-856-320A-2_COPY_54_282 (1-229) x AAZ89012 (1-180)

QY 21 LysThrArgLeuLeuCysGlyAlaThrLeuLeuAlaProArgTrpLeuLeuThrAlaAla 40
 Db 1 AAAGTTGAGGCGTCTCTGTGGAGTCTATCATTAATGAATAATGGTCGTAACTCAGGCC 60

QY 41 HisCysLeuLysPro-----ArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLys 58
 Db 61 CACTGTATCAAAACCGGATGATAATATTACAGTTCTTCAGGTGAATATAACATTTCAGGAG 120

QY 59 GluGluGlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsn 78
 Db 121 ACTGGAATACAGAGCAAGGAAATGTGATTGGAATTATTCCTTACCACAAATACAA 180

RESULT 37

ABV38147/c

ID ABV38147 standard; cDNA; 179 BP.

XX AC ABV38147;

XX DT 16-SEP-2002 (first entry)

XX DE Human prostate expression marker cDNA 38138.

XX KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;

XX KW pharmacogenomic marker; gene; ss.

XX OS Homo sapiens.

XX PN WO200160860-A2.

XX PD 23-AUG-2001.

XX PF 20-FEB-2001; 2001WO-US005171.

XX PR 17-FEB-2000; 2000US-0183319P.

XX PR 16-MAR-2000; 2000US-0189862P.

XX PR 25-MAY-2000; 2000US-0207454P.

XX PR 09-JUN-2000; 2000US-0211314P.

XX PR 18-JUL-2000; 2000US-0219007P.

XX PR 13-DEC-2000; 2000US-0255281P.

XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX PI Schlegel R, Endege WO, Monahan JE;

XX DR WPI; 2001-662795/76.

XX PT Novel isolated nucleic acid molecule associated with cancerous state of

XX prostate cells and correlating with presence of prostate cancer, useful

XX for detecting presence of prostate cancer, stage of prostate cancer.

XX PS Claim 1; Page 7788; 11750pp; English.

XX CC The invention relates to an isolated nucleic acid molecule (I) comprising

XX a nucleotide sequence given in tables 1-9 (ABV00010-ABV62213) of the

XX specification or its complement. (I) is useful for: (a) assessing whether

XX a patient is afflicted with prostate cancer; (b) monitoring the

XX progression of prostate cancer in a patient; (c) assessing the efficacy

XX of a test compound to inhibit prostate cancer in a patient; (d) assessing

XX the efficacy of a therapy for inhibiting prostate cancer in a patient;

XX (e) selecting a composition for inhibiting prostate cancer in a patient;

XX (f) assessing the prostate cell carcinogenic potential of a compound; (g)

XX determining whether prostate cancer has metastasized in a patient; (h)

XX assessing the aggressiveness or indolence of prostate cancer in a patient

XX ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker

XX

SQ Sequence 179 BP; 37 A; 51 C; 55 G; 36 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0.0201 Length: 179

Score: 120.50 Matches: 21

Percent Similarity: 62.79% Conservative: 6
 Best Local Similarity: 48.84% Mismatches: 9
 Query Match: 9.58% Indels: 7
 DB: 5 Gaps: 1

US-09-856-320a-2_COPY_54_282 (1-229) x ABV38147 (1-179)

Qy 183 GlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGlnAspPro 202
 Db 179 GGGGGCCCACTTGTCTGTANTGCTGCTTCAGGTATACAGTCATCGGGCAGTGAACCA 120
 Qy 203 CysAlaIleThrArgLysProGlyValTyrThr-----LysVal 215
 Db 119 TGTGCCCTGCCGAAAGGCTTCCCTGTACCTCGCGCGGACACGCTAAGGGCGGAATTC 60
 Qy 216 CysLysTyr 218
 Db 59 TGCAGATAT 51

RESULT 38

ABV44351/C
 ID ABV44351 standard; cDNA; 179 BP.

XX AC ABV44351;

XX DT 16-SEP-2002 (first entry)

XX DE Human prostate expression marker cDNA 44342.

XX KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW Pharmacogenomic marker; gene; ss.

XX OS Homo sapiens.

XX FN WO200160860-A2.

XX PD 23-AUG-2001.

XX PF 20-FEB-2001; 2001WO-US005171.

XX PR 17-FEB-2000; 2000US-0183319P.

XX PR 16-MAR-2000; 2000US-0189862P.

XX PR 25-MAY-2000; 2000US-0207454P.

XX PR 09-JUN-2000; 2000US-0211314P.

XX PR 18-JUL-2000; 2000US-0219007P.

XX PR 13-DEC-2000; 2000US-0255281P.

XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX PI Schlegel R, Endege WO, Monahan JE;

XX DR WPI; 2001-662795/76.

XX PS Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer.

XX PS Claim 1; Page 8804; 11750pp; English.

XX CC The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification or its complement. (I) is useful for: (a) assessing whether
 CC a patient is afflicted with prostate cancer; (b) monitoring the
 CC progression of prostate cancer in a patient; (c) assessing the efficacy
 CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
 CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
 CC determining whether prostate cancer has metastasized in a patient; (h)
 CC assessing the aggressiveness or indolence of prostate cancer in a patient
 CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker

XX SQ Sequence 179 BP; 37 A; 51 C; 55 G; 36 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0.0201 Length: 179
 Score: 120.50 Matches: 21
 Percent Similarity: 62.79% Conservative: 6
 Best Local Similarity: 48.84% Mismatches: 9
 Query Match: 9.58% Indels: 7
 DB: 5 Gaps: 1

US-09-856-320a-2_COPY_54_282 (1-229) x ABV44351 (1-179)

Qy 183 GlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGlnAspPro 202
 Db 179 GGGGGCCCACTTGTCTGTANTGCTGCTTCAGGTATACAGTCATCGGGCAGTGAACCA 120
 Qy 203 CysAlaIleThrArgLysProGlyValTyrThr-----LysVal 215
 Db 119 TGTGCCCTGCCGAAAGGCTTCCCTGTACCTCGCGCGGACACGCTAAGGGCGGAATTC 60

Qy 216 CysLysTyr 218

Db 59 TGCAGATAT 51

RESULT 39

AAD58752
 ID AAD58752 standard; DNA; 172 BP.

XX AC AAD58752;

XX DT 04-DEC-2003 (first entry)

XX DE Human transmembrane serine protease (TSP1-TSP34) gene exon 7.

XX KW Human; transmembrane serine protease; TSP; therapy; immunogen; cancer;
 KW autoimmune disease; immunomodulatory; immunosuppressive; enzyme; ds.

XX OS Homo sapiens.

XX FN WO2003064641-A1.

XX PD 07-AUG-2003.

XX PF 24-JAN-2003; 2003WO-EP000756.

XX PR 30-JAN-2002; 2002US-0352806P.

XX PA (GENE-) GENEPROT INC.

XX PI Bougueleret L, Niknejad A, Saudrais C;

XX DR WPI; 2003-627608/59.

XX PT New purified transmembrane serine protease polypeptides (TSP1-TSP34)
 PT comprising a protease domain or its biologically active portion, useful
 PT for identifying modulators of proteolysis.

XX PS Claim 6; Page 229; 276pp; English.

XX CC The invention relates to purified human transmembrane serine protease
 CC (TSP) polypeptide, comprising a protease domain of a type-II membrane-
 CC type serine protease or its biologically active portion. The invention is
 CC useful for cleaving a TSP substrate protein by contacting TSP with a
 CC substrate protein under serine protease activity permissive conditions.
 CC The invention is useful as an immunogen to generate antibodies that bind
 CC TSP or TSP1-TSP34 proteins, useful for treating disease e.g. cancer and
 CC autoimmune disease. The present sequence is human TSP1-TSP34 gene exon.

XX SQ Sequence 172 BP; 31 A; 46 C; 61 G; 34 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0.0395 Length: 172
 Score: 117.00 Matches: 21
 Percent Similarity: 61.90% Conservative: 5

Best Local Similarity: 50.00% Mismatches: 16
 Query Match: 9.30% Indels: 0
 DB: 8 Gaps: 0

US-09-856-320A-2_COPY_54_282 (1-229) x AAD58752 (1-172)

Qy 1 IleIleLysGlyPheGluCysLysProHisSerGlnProTrpGlnAlaLeuPheGlu 20
 Db 39 ATCTGGCGCGCATGGAAGCATCCCGGGGAGTTCCGTTGGCAAGCCCTTCGAGAG 98
 Qy 21 LysThrArgLeuLeuCysGlyAlaThrLeuLeuAlaProArgTrpLeuLeuThrAlaAla 40
 Db 99 AACAGAGACATCTCTGTGGGGCGCCATCATCAAGCCAGGTGGCTGGTGTCTGTCT 158
 Qy 41 HisCys 42
 Db 159 CACTGC 164

RESULT 40

AAZ89007
 ID AAZ89007 standard; DNA; 180 BP.

XX AC AAZ89007;

DT 02-JUN-2000 (first entry)

DE Human Factor IX DNA fragment.

XX KW RAWIT; RNA amplification with in vitro translation; RAWTS; Factor IX;
 KW RNA amplification with transcript sequencing; human; ss.

XX OS Homo sapiens.

XX FN US6027913-A.

XX PD 22-FEB-2000.

XX PF 27-DEC-1994; 94US-00399855.

XX PR 28-JAN-1988; 88US-00149312.

XX PR 24-JUL-1989; 89US-00385013.

XX PR 12-NOV-1993; 93US-00151461.

XX PA (SOMM/) SOMMER S S.

XX PI Sommer SS;

XX DR WPI; 2000-194830/17.

XX DR P-PSDB; AAY51617.

XX PT Producing polypeptides from nucleic acid sequences of interest using a
 XX modified RAWIT (RNA amplification with in vitro translation) method.

XX PS Disclosure; Fig 4; 65pp; English.

XX CC This invention describes a novel modified RAWIT (RNA amplification with
 CC in vitro translation) method, for synthesizing polypeptides encoded by
 CC sequences of interest. The method generates a protein from an RNA
 CC molecule and comprises (a) incubating the RNA with reverse transcriptase
 CC to form cDNA; (b) amplifying the cDNA of step (a) to generate DNA copies
 CC of the cDNA in the presence of at least 1 oligonucleotide primer which
 CC contains an RNA promoter sequence; (c) transcribing the DNA generated
 CC with an RNA polymerase to form RNA transcripts; and (d) translating the
 CC RNA transcripts in vitro to generate the protein. This sequence encodes a
 CC fragment of the human Factor IX protein which is used to illustrate the
 CC RAWTS (RNA amplification with transcript sequencing) method of the
 CC invention

SQ Sequence 180 BP; 62 A; 30 C; 39 G; 49 T; 0 U; 0 Other;

Alignment Scores: 0.0419 Length: 180
 Pred. No.: 117.00 Matches: 20
 Score:

Percent Similarity: 56.67% Conservative: 14
 Best Local Similarity: 33.33% Mismatches: 24
 Query Match: 9.30% Indels: 2
 DB: 3 Gaps: 1

US-09-856-320A-2_COPY_54_282 (1-229) x AAZ89007 (1-180)

Qy 21 LysThrArgLeuLeuCysGlyAlaThrLeuLeuAlaProArgTrpLeuLeuThrAlaAla 40
 Db 1 AAAGTTGATGATCTCTGTGGAGGCTCTATCGTTAATGAAAAATGATTAACCTGCTGCC 60

Qy 41 HisCysLeuLysPro-----ArgTyrIleValHisLeuGlnHisAsnLeuGlnLys 58
 Db 61 CACTGTGTGTAAGAACTGTTTAAATAATTACAGTTTCGAGGTGAACATAATAATTGAGGAG 120

Qy 59 GluGluGlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsn 78
 Db 121 ACAGAACATACAGAGCAAAAGCGAAATGTGATTGGAATTATTCCTCACCACACTACAT 180

RESULT 41

AAZ89007

ID AAD58758 standard; DNA; 172 BP.

XX AC AAD58758;

XX DT 04-DEC-2003 (first entry)

DE Human transmembrane serine protease (TSP1-TSP34) gene exon 11.

XX KW Human; transmembrane serine protease; TSP; therapy; immunogen; cancer;
 KW autoimmune disease; immunomodulatory; immunosuppressive; enzyme; ds.

XX OS Homo sapiens.

XX FN WO2003064641-A1.

XX PD 07-AUG-2003.

XX PF 24-JAN-2003; 2003WO-EP000756.

XX PR 30-JAN-2002; 2002US-0352806P.

XX PA (GENE-) GENEPROT INC.

XX PI Bougueleret L, Niknejad A, Saudrais C;

XX DR WPI; 2003-627608/59.

XX PT New purified transmembrane serine protease polypeptides (TSP1-TSP34)
 XX comprising a protease domain or its biologically active portion, useful
 XX for identifying modulators of proteolysis.

XX PS Claim 6; Page 232; 276pp; English.

XX CC The invention relates to purified human transmembrane serine protease
 CC (TSP) polypeptide, comprising a protease domain of a type-II membrane-
 CC type serine protease or its biologically active portion. The invention is
 CC useful for cleaving a TSP substrate protein by contacting TSP with a
 CC substrate protein under serine protease activity permissive conditions.
 CC The invention is useful as an immunogen to generate antibodies that bind
 CC TSP or TSP1-TSP34 proteins, useful for treating disease e.g. cancer and
 CC autoimmune disease. The present sequence is human TSP1-TSP34 gene exon
 XX Sequence 172 BP; 26 A; 51 C; 66 G; 29 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0.0486 Length: 172
 Score: 116.00 Matches: 20
 Percent Similarity: 64.29% Conservative: 7
 Best Local Similarity: 47.62% Mismatches: 15
 Query Match: 9.22% Indels: 0
 DB: 8 Gaps: 0


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QY 195 llelleSerTrpGlyGlnAspProCysAlaIalleThrArgLysProGlyValTyThrLys 214
DB 61 ATTGAAGCTGGGA--GATAACTGTGGTCAAAAGGACCAAGCTGGAGTCTACACAA 117
QY 215 ValCysLysTyValAspTrpIle 222
DB 118 GTGACTTATTACCGAAACTGGATT 141

RESULT 44
AAK21293
ID AAK21293 standard; DNA; 162 BP.
XX
AC AAK21293;
XX
DT 05-NOV-2001 (first entry)
XX
DE Human brain expressed single exon probe SEQ ID NO: 21284.
XX
KW Human; brain expressed exon; gene expression analysis; probe; microarray;
KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
KW ss.
XX
OS Homo sapiens.
XX
PN WO200157275-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US0000667.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-483446/52.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
PT brains.
XX
PS Example 4; SEQ ID NO 21284; 650pp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is one of the probes of the
CC invention
XX
SQ Sequence 162 BP; 51 A; 28 C; 43 G; 40 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0.0554 Length: 162
Score: 115.00 Matches: 26
Percent Similarity: 60.42% Conservative: 3
Best Local Similarity: 54.17% Mismatches: 13
Query Match: 9.14% Indels: 6
DB: Gaps: 2

US-09-856-320A-2_COPY_54_282 (1-229) x AAK21293 (1-162)

QY 180 GlyAspSerGlyGlyProLeuValCysAsnGln-----SerLeuGlnGly 194
DB 1 GGTGATTCTGGGGGACCTTTTATGACCAAGGAGTCAAGGATCGTGGTATCTCATTTGGA 60

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QY 195 llelleSerTrpGlyGlnAspProCysAlaIalleThrArgLysProGlyValTyThrLys 214
DB 61 ATTGAAGCTGGGA--GATAACTGTGGTCAAAAGGACCAAGCTGGAGTCTACACAA 117
QY 215 ValCysLysTyValAspTrpIle 222
DB 118 GTGACTTATTACCGAAACTGGATT 141

RESULT 45
ABS47188
ID ABS47188 standard; DNA; 162 BP.
XX
AC ABS47188;
XX
DT 25-FEB-2003 (first entry)
XX
DE Human liver single exon probe, SEQ ID NO 22178.
XX
KW Human; single exon nucleic acid probe; liver; cirrhosis;
KW hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;
KW coronary heart disease; ss.
XX
OS Homo sapiens.
XX
PN WO200157273-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US0000664.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488898/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human adult liver.
XX
PS Claim 4; SEQ ID NO 22178; 658pp; English.
XX
CC The invention relates to a single exon nucleic acid probe (SENP) (I) for
CC measuring human gene expression in a sample derived from human adult
CC liver, comprising one of 13109 defined nucleotide sequences given in the
CC specification (or complements/ fragments). The probe hybridises at high
CC stringency to a nucleic acid molecule expressed in the human adult liver.
CC (I) may be used for predicting, measuring and displaying gene expression
CC in samples derived from human adult liver. The genes identified may be
CC involved in genetic liver diseases such as cirrhosis,
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
CC associated with coronary heart disease. ABS25011-ABS51005 represent human
CC liver single exon nucleic acid probes of the invention. Note: The
CC sequence information for this patent does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 162 BP; 51 A; 28 C; 43 G; 40 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0.0554 Length: 162
Score: 115.00 Matches: 26
Percent Similarity: 60.42% Conservative: 3
Best Local Similarity: 54.17% Mismatches: 13
Query Match: 9.14% Indels: 6

```

DB: 4 Gaps: 2
US-09-856-320A-2_COPY_54_282 (1-229) x ABS47188 (1-162)
QY 180 GIVAspSerGlyGlyProLeuValCysAsnGln-----SerLeuGlnCly 194
DB 1 GGTGATCTGGGGACCTTTAGTTCACAGGATCTGAAGATACGTGGTATCATTGGA 60
QY 195 IleleSerTrpGlyGlnAspProCysAlaIleThrArgLysProGlyValTyThrLys 214
DB 61 ATTGTAACTGGGA--GATAACTGTGTGTTCAAAAGGACACAGCTGGAGTGTACACAA 117
QY 215 ValCysLysTyTrValAspTrpIle 222
DB 118 GTGACTTATTACCGAAACTGGATT 141
RESULT 46
ID ABV97886/c
ID ABV97886 standard; cDNA; 184 BP.
XX AC ABV97886;
XX 14-JAN-2003 (first entry)
XX Human pancreatic cancer expressed cDNA SEQ ID NO 3294.
XX Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;
XX cytostatic; tumour; gene; ss.
XX Homo sapiens.
XX WO200260317-A2.
XX 08-AUG-2002.
XX 30-JAN-2002; 2002WO-US002781.
XX 30-JAN-2001; 2001US-0265305P.
XX 31-JAN-2001; 2001US-0265682P.
XX 09-FEB-2001; 2001US-0267568P.
XX 21-MAR-2001; 2001US-0278651P.
XX 28-APR-2001; 2001US-0287112P.
XX 16-MAY-2001; 2001US-0291631P.
XX 12-JUL-2001; 2001US-0305484P.
XX 20-AUG-2001; 2001US-0313999P.
XX 27-NOV-2001; 2001US-0333626P.
XX (CORI-) CORIXA CORP.
XX Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y;
XX WPI; 2002-627435/67.
XX New isolated polynucleotide and pancreatic tumor polypeptides, useful for
XX diagnosing, preventing and/or treating cancer, particularly pancreatic
XX cancer.
XX Claim 1; SEQ ID NO 3294; 300pp + Sequence Listing; English.
XX The invention relates to an isolated polynucleotide (I) comprising: (a)
XX any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b)
XX complements of (a); (c) sequences consisting of at least 20 contiguous
XX residues of (a); (d) sequences that hybridize to (a), under moderately
XX stringent conditions; (e) sequences having at least 75% or 90% identity
XX to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-
XX ABP68637) encoded by (I) and oligonucleotide can be used to detect cancer
XX in a patient and compositions comprising polypeptides, polynucleotides,
XX antibodies, fusion proteins, T cell populations and antigen presenting
XX cells expressing the polypeptide are useful in treating pancreatic cancer
XX and stimulating an immune response. The polynucleotides can be used as
XX probes or primers for nucleic acid hybridisation, in the design and
XX preparation of ribozyme molecules for inhibiting expression of the tumour
XX polypeptides and proteins in the tumour cells, in vaccines and for gene

CC therapy. Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 184 BP; 41 A; 59 C; 53 G; 31 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 0.0803 Length: 184
Score: 114.00 Matches: 24
Percent Similarity: 61.02% Conservative: 12
Best Local Similarity: 40.68% Mismatches: 17
Query Match: 9.06% Indels: 6
DB: Gaps: 3
US-09-856-320A-2_COPY_54_282 (1-229) x ABV97886 (1-184)
QY 1 IleleLysGlyPheGluCysLysProHisSerGlnProTrpGlnAlaAlaLeu---Phe 19
DB 178 GTTGTCAATGGTGAAGATCGGTCCCTACAGCTGGCCCTGGCAGGTTTCCCTGCAGTAT 119
QY 20 GluLysThrArgLeuLeu-----CysGlyAlaThrLeuIleAlaProArgTrpLeu 36
DB 118 GAGAAAGTGAAGCTTCTACACACAGTGTGGGGTAGCTCATCGCCCGCAGTGGTT 59
QY 37 LeuThrAlaAlaHisCysLeuLysPro-----ArgTyIleValHisLeuGlyGln 53
DB 58 GTGACTGCGCGGCACGCTCATCTCGAGCTCTCGAGCTCTCGAGCTGTGTGGCGCGAG 2
RESULT 47
ID ABV98082
ID ABV98082 standard; cDNA; 195 BP.
XX AC ABV98082;
XX 14-JAN-2003 (first entry)
XX Human pancreatic cancer expressed cDNA SEQ ID NO 3490.
XX Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;
XX cytostatic; tumour; gene; ss.
XX Homo sapiens.
XX WO200260317-A2.
XX 08-AUG-2002.
XX 30-JAN-2002; 2002WO-US002781.
XX 30-JAN-2001; 2001US-0265305P.
XX 31-JAN-2001; 2001US-0265682P.
XX 09-FEB-2001; 2001US-0267568P.
XX 21-MAR-2001; 2001US-0278651P.
XX 28-APR-2001; 2001US-0287112P.
XX 16-MAY-2001; 2001US-0291631P.
XX 12-JUL-2001; 2001US-0305484P.
XX 20-AUG-2001; 2001US-0313999P.
XX 27-NOV-2001; 2001US-0333626P.
XX (CORI-) CORIXA CORP.
XX Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y;
XX WPI; 2002-627435/67.
XX New isolated polynucleotide and pancreatic tumor polypeptides, useful for
XX diagnosing, preventing and/or treating cancer, particularly pancreatic
XX cancer.
XX Claim 1; SEQ ID NO 3490; 300pp + Sequence Listing; English.
XX The invention relates to an isolated polynucleotide (I) comprising: (a)
XX any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b)
XX complements of (a); (c) sequences consisting of at least 20 contiguous
XX residues of (a); (d) sequences that hybridize to (a), under moderately
XX stringent conditions; (e) sequences having at least 75% or 90% identity
XX to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-
XX ABP68637) encoded by (I) and oligonucleotide can be used to detect cancer
XX in a patient and compositions comprising polypeptides, polynucleotides,
XX antibodies, fusion proteins, T cell populations and antigen presenting
XX cells expressing the polypeptide are useful in treating pancreatic cancer
XX and stimulating an immune response. The polynucleotides can be used as
XX probes or primers for nucleic acid hybridisation, in the design and
XX preparation of ribozyme molecules for inhibiting expression of the tumour
XX polypeptides and proteins in the tumour cells, in vaccines and for gene

CC complements of (a); (c) sequences consisting of at least 20 contiguous
 CC residues of (a); (d) sequences that hybridize to (a), under moderately
 CC stringent conditions; (e) sequences having at least 75% or 90% identity
 CC to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-
 CC ABP68637) encoded by (i) and oligonucleotide can be used to detect cancer
 CC in a patient and compositions comprising polypeptides, polynucleotides,
 CC antibodies, fusion proteins, T cell populations and antigen presenting
 CC cells expressing the polypeptide are useful in treating pancreatic cancer
 CC and stimulating an immune response. The polynucleotides can be used as
 CC probes or primers for nucleic acid hybridisation, in the design and
 CC preparation of ribozyme molecules for inhibiting expression of the tumour
 CC polypeptides and proteins in the tumour cells, in vaccines and for gene
 CC therapy. Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 195 BP; 31 A; 59 C; 60 G; 45 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 0.0864 Length: 195
 Score: 114.00 Matches: 24
 Percent Similarity: 61.02% Conservative: 12
 Best Local Similarity: 40.68% Mismatches: 17
 Query Match: 9.06% Indels: 6
 DB: Gaps: 3

US-09-856-320A-2_COPY_54_282 (1-229) x ABV98082 (1-195)

QY 1 IlelelysglypheGluCysLysProHisSerGlnProTrpGlnAlaLeu---Phe 19
 Db 18 GTTGTCAATGGTGAGGATCGGTCCTACAGCTGGCCCTGGCAGGTTTCCTCGCAGTAT 77
 QY 20 GlutylsthrArgLeuLeu-----CysGlyAlaThrLeuLeuAlaProArgTrpLeu 36
 Db 78 GAGAAAGTGGAGCTTCTACACACGTGGGGGGTAGCTCTATCGCCCGCAGTGGGTT 137
 QY 37 LeuThrAlaAlaHisCysLeuLysPro-----ArgTyrIleValHisLeuGlyGln 53
 Db 138 GTGACTCGCGGCCACTGCTATCGAGCTCTCGAGCTCTCGACCTACACAGTGGTGTGGTGAG 194

RESULT 48
 ABV98457
 ID ABV98457 standard; cDNA; 214 BP.
 XX
 AC ABV98457;
 XX
 XX 14-JAN-2003 (first entry)
 XX
 DE Human pancreatic cancer expressed cDNA SEQ ID NO 3865.
 XX
 XX Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;
 KW cytosolic; tumour; gene; ss.
 XX
 OS Homo sapiens.
 XX
 XX W0200260317-A2.
 XX
 XX 08-AUG-2002.
 XX
 XX 30-JAN-2002; 2002WO-US002781.
 XX
 PR 30-JAN-2001; 2001US-0265305P.
 PR 31-JAN-2001; 2001US-0265582P.
 PR 09-FEB-2001; 2001US-0267568P.
 PR 21-MAR-2001; 2001US-0278651P.
 PR 28-APR-2001; 2001US-0287112P.
 PR 15-MAY-2001; 2001US-0291631P.
 PR 12-JUL-2001; 2001US-0305484P.
 PR 20-AUG-2001; 2001US-0313999P.
 PR 27-NOV-2001; 2001US-0333626P.
 XX
 XX (CORI-) CORIXA CORP.

PI Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y;
 XX WPI; 2002-627435/67.
 XX
 XX New isolated polynucleotide and pancreatic tumor polypeptides, useful for
 PT diagnosing, preventing and/or treating cancer, particularly pancreatic
 PT cancer.
 XX
 PS Claim 1; SEQ ID NO 3865; 300pp + Sequence Listing; English.

XX The invention relates to an isolated polynucleotide (I) comprising: (a)
 CC any of a group of over 4000 nucleotide sequences (ABV9428-ABV99145); (b)
 CC complements of (a); (c) sequences consisting of at least 20 contiguous
 CC residues of (a); (d) sequences that hybridize to (a), under moderately
 CC stringent conditions; (e) sequences having at least 75% or 90% identity
 CC to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-
 CC ABP68637) encoded by (i) and oligonucleotide can be used to detect cancer
 CC in a patient and compositions comprising polypeptides, polynucleotides,
 CC antibodies, fusion proteins, T cell populations and antigen presenting
 CC cells expressing the polypeptide are useful in treating pancreatic cancer
 CC and stimulating an immune response. The polynucleotides can be used as
 CC probes or primers for nucleic acid hybridisation, in the design and
 CC preparation of ribozyme molecules for inhibiting expression of the tumour
 CC polypeptides and proteins in the tumour cells, in vaccines and for gene
 CC therapy. Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX

SQ Sequence 214 BP; 33 A; 68 C; 64 G; 49 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 0.0973 Length: 214
 Score: 114.00 Matches: 24
 Percent Similarity: 61.02% Conservative: 12
 Best Local Similarity: 40.68% Mismatches: 17
 Query Match: 9.06% Indels: 6
 DB: Gaps: 3

US-09-856-320A-2_COPY_54_282 (1-229) x ABV98457 (1-214)

QY 1 IlelelysglypheGluCysLysProHisSerGlnProTrpGlnAlaLeu---Phe 19
 Db 37 GTTGTCAATGGTGAGGATCGGTCCTACAGCTGGCCCTGGCAGGTTTCCTCGCAGTAT 96
 QY 20 GlutylsthrArgLeuLeu-----CysGlyAlaThrLeuLeuAlaProArgTrpLeu 36
 Db 97 GAGAAAGTGGAGCTTCTACACACGTGGGGGGTAGCTCTATCGCCCGCAGTGGGTT 156
 QY 37 LeuThrAlaAlaHisCysLeuLysPro-----ArgTyrIleValHisLeuGlyGln 53
 Db 157 GTGACTCGCGGCCACTGCTATCGAGCTCTCGAGCTCTCGACCTACACAGTGGTGTGGTGAG 213

RESULT 49
 AAA64312/C
 ID AAA64312 standard; DNA; 94 BP.
 XX
 AC AAA64312;
 XX
 XX 20-DEC-2000 (first entry)
 XX
 DE PCR primer for a protein C activator polypeptide DNA fragment.
 XX
 KW Protein C activator; PCA; venom; snake; blood coagulation; factor VIIa;
 KW activated protein C; APC; anticoagulant; Factor Va; clot formation;
 KW trypsin-type serine protease; blood coagulation factor; PCR primer; ss.
 OS Agkistrodon contortrix contortrix.
 XX
 XX W0200050612-A2.
 XX
 XX 31-AUG-2000.
 XX
 XX 22-FEB-2000; 2000WO-US004406.


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XX 22-FEB-1999; 99US-0121121P.
XX (INLI ) INSTRUMENTATION LAB.
XX Kunes YZ, Sanz M, Tumanova IA, Birr CA, Shi PQ, Bruguera P;
XX Ruiz JA, Sanchez-Martinez D;
XX WPI; 2000-543915/49.
XX
XX Pure protein C activator (PCA) preparation comprising a PCA protein with
XX a defined sequence found in Agkistrodon contortrix Confortrix (ACC)
XX venom, useful for evaluating the level or activity of blood coagulation
XX factors.
XX Example; Page 46; 47pp; English.
XX
XX PCR primers AAA64311-14 were used to amplify a fragment of DNA encoding a
XX protein C activator (PCA). The polypeptide is found in the venom of the
XX snake Agkistrodon contortrix Confortrix. PCA is an enzyme in the blood
XX coagulation pathway that is normally activated by a complex series of
XX events to become activated protein C (APC). APC has an anticoagulant
XX effect by inactivating Factors Va and VIIIa, and thereby slowing the
XX conversion of fibrinogen to fibrin and clot formation. The PCA of the
XX invention is a trypsin-type serine protease. The PCA protein is useful in
XX diagnostic kits for evaluating the level or activity of blood coagulation
XX factors
XX
XX Sequence 94 BP; 28 A; 20 C; 21 G; 25 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 0.042 Length: 94
XX Score: 113.00 Matches: 20
XX Percent Similarity: 77.42% Conservative: 4
XX Best Local Similarity: 64.52% Mismatches: 7
XX Query Match: 8.98% Indels: 0
XX DB: 3 Gaps: 0
XX
XX US-09-856-320A-2_COPY_54_282 (1-229) x AAA64312 (1-94)
XX
XX QY 185 ProLeuValCysAndInSerLeuGlnGlyIleIleSerTrpGlyGlnAspProCysAla 204
XX Db 93 CCATTGATCTGTAAACGGTCAATTCGAAGGTATCTTCTGTTGGTGAACCCATGTGCT 34
XX
XX QY 205 IleThrArgLysProGlyValTyrThrLysVal 215
XX Db 33 CAACCAAGAAAGCCAGGTAATACATAAGTTT 1
XX
XX RESULT 50
XX ABV98446/c
XX ID ABV98446 standard; cDNA; 205 BP.
XX
XX AC ABV98446;
XX
XX DT 14-JAN-2003 (first entry)
XX
XX DE Human pancreatic cancer expressed cDNA SEQ ID NO 3854.
XX
XX KW Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;
XX cytostatic; tumour; gene, ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200260317-A2.
XX
XX PD 08-AUG-2002.
XX
XX PF 30-JAN-2002; 2002WO-US002781.
XX
XX PR 30-JAN-2001; 2001US-0265305P.
XX PR 31-JAN-2001; 2001US-0265682P.
XX PR 09-FEB-2001; 2001US-0267568P.
XX PR 21-MAR-2001; 2001US-0278651P.
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PR 28-APR-2001; 2001US-0287112P.
PR 16-MAY-2001; 2001US-0291631P.
PR 12-JUL-2001; 2001US-0305484P.
PR 20-AUG-2001; 2001US-0313999P.
PR 27-NOV-2001; 2001US-0333626P.
XX (CORI-) CORIXA CORP.
XX
XX Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y;
XX WPI; 2002-627435/67.
XX
XX New isolated polynucleotide and pancreatic tumor polypeptides, useful for
XX diagnosing, preventing and/or treating cancer, particularly pancreatic
XX cancer.
XX
XX Claim 1; SEQ ID NO 3854; 300pp + Sequence Listing; English.
XX
XX The invention relates to an isolated polynucleotide (I) comprising: (a)
XX any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b)
XX complements of (a); (c) sequences consisting of at least 20 contiguous
XX residues of (a); (d) sequences that hybridize to (a), under moderately
XX stringent conditions; (e) sequences having at least 75% or 90% identity
XX to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-
XX ABP68637) encoded by (I) and oligonucleotide can be used to detect cancer
XX in a patient and compositions comprising polypeptides, polynucleotides,
XX antibodies, fusion proteins, T cell populations and antigen presenting
XX cells expressing the polypeptide are useful in treating pancreatic cancer
XX and stimulating an immune response. The polynucleotides can be used as
XX probes or primers for nucleic acid hybridization, in the design and
XX preparation of ribozyme molecules for inhibiting expression of the tumour
XX polypeptides and proteins in the tumour cells, in vaccines and for gene
XX therapy. Note: The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 205 BP; 49 A; 61 C; 61 G; 33 T; 0 U; 1 Other;
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Alignment Scores:

Pred. No.:	0.113	Length:	205
Score:	113.00	Matches:	24
Percent Similarity:	61.02%	Conservative:	12
Best Local Similarity:	40.68%	Mismatches:	17
Query Match:	8.98%	Indels:	5
DB:	6	Gaps:	3

US-09-856-320A-2_COPY_54_282 (1-229) x ABV98446 (1-205)

QY	1	IleIleLysGlyPheGluCysLysProHisSerGlnProTrpGlnAlaAlaLeu---	Phe 19
Db	178	GTTCGTCATGCTGAGGATGCGGTCCCTACAGTCGGCCCTGGCAGGTTCCCTGCAGTAT	119
QY	20	GluLysThrArgLeuLeu-----CysGlyAlaThrLeuIleAlaProA:GTrpLeu	36
Db	118	CAGAAAAGTGGAGCTTCTACACANGTGTGGGGTAGCCTCATCGCCCGATGGGTT	59
QY	37	LeuThrAlaAlaHisCysLeuLysPro-----ArgTyrIleValHisLeuGlyGln	53
Db	58	GTGATCCCGGCCACTGCATCTCGAGGGATCTGACCTACCCAGGTTGTTGGTGAG	2

Search completed: June 27, 2004, 00:25:32

Job time : 476 secs

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